

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992

Sequence: 1 MHFTQVLISLVLIACGPGV.....KEQIIYKIPSMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284.5	14.3	391	1	US-10-517-544-77
2	253	12.7	431	1	US-10-816-768-39
3	237	11.9	366	7	US-11-091-334-9
4	233	11.7	203	1	US-10-816-768-100
5	227.5	11.4	102	1	US-10-816-768-47
6	227.5	11.4	102	1	US-10-816-768-85
7	226.5	11.4	102	1	US-10-816-768-86
8	225.5	11.3	102	1	US-10-816-768-46
9	224.5	11.3	102	1	US-10-816-768-84
10	224	11.2	117	1	US-10-816-768-69
11	224	11.2	139	1	US-10-816-768-68
12	224	11.2	364	1	US-10-131-826A-342
13	224	11.2	364	7	US-11-091-334-2
14	223.5	11.2	102	1	US-10-816-768-88
15	223.5	11.2	129	1	US-10-816-768-89
16	223	11.2	429	1	US-10-967-457-74
17	220.5	11.1	102	1	US-10-816-768-53
18	219.5	11.0	106	1	US-10-816-768-62
19	219.5	11.0	106	1	US-10-816-768-63
20	216.5	10.9	102	1	US-10-816-768-83
21	216.5	10.9	102	1	US-10-816-768-87
22	212.5	10.7	98	1	US-10-816-768-41
23	212	10.6	101	1	US-10-816-768-49
24	211.5	10.6	98	1	US-10-816-768-42
25	211.5	10.6	102	1	US-10-816-768-55

26	210	10.5	101	1	US-10-816-768-59	Sequence 59, Appl
27	207.5	10.4	102	1	US-10-816-768-52	Sequence 52, Appl
28	204.5	10.3	102	1	US-10-816-768-56	Sequence 56, Appl
29	200	10.0	101	1	US-10-816-768-51	Sequence 51, Appl
30	198	9.9	103	1	US-10-816-768-50	Sequence 50, Appl
31	197.5	9.9	102	1	US-10-816-768-45	Sequence 45, Appl
32	196.5	9.9	98	1	US-10-816-768-44	Sequence 44, Appl
33	195.5	9.8	98	1	US-10-816-768-43	Sequence 43, Appl
34	189.5	9.5	98	1	US-10-816-768-64	Sequence 64, Appl
35	188.5	9.5	98	1	US-10-816-768-40	Sequence 40, Appl
36	185	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
37	181.5	9.1	102	1	US-10-816-768-57	Sequence 57, Appl
38	180.5	9.1	118	1	US-10-816-768-48	Sequence 48, Appl
39	176	8.8	35	1	US-10-816-768-9	Sequence 9, Appl
40	166	8.3	103	1	US-10-816-768-54	Sequence 54, Appl
41	147.5	7.4	102	1	US-10-816-768-60	Sequence 60, Appl
42	125.5	6.3	104	1	US-10-816-768-65	Sequence 65, Appl
43	116	5.8	105	1	US-10-816-768-61	Sequence 61, Appl
44	113	5.7	39	1	US-10-816-768-115	Sequence 115, App
45	111	5.6	39	1	US-10-816-768-119	Sequence 119, App

ALIGNMENTS

RESULT 1

US-10-517-544-77

; Sequence 77, Application US/10517544

; Publication No. US20050250100A1

; GENERAL INFORMATION:

; APPLICANT: RIKEN

; APPLICANT: KABUSHIKI KAISHA DNAFORM

; TITLE OF INVENTION: Method for utilizing the 5'end of mRNA for cloning and analysis

; FILE REFERENCE: 1336(PCT)

; CURRENT APPLICATION NUMBER: US/10/517,544

; PRIOR FILING DATE: 2004-12-10

; PRIOR APPLICATION NUMBER: JP 2002-171851

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: JP 2002-235294

; PRIOR FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 77

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-517-544-77

Query Match	14.3%;	Score 284.5;	DB 1;	Length 391;
Best Local Similarity	25.9%;	Pred. No. 1.1e-22;		
Matches	97;	Conservative	66;	Mismatches 157; Indels 55; Gaps 14;
Qy	41	STCEP--RHSKLMRLHAITSQILSKRLKQAPNISRDVVKQLLPKAPPLQQLDQD--	96	
Db	31	STCKTDMELVKRIEIRGQILSKRLASPSQGE-----VPPGPLPEAVLALYNST	84	
Qy	97	---VLGDDSKDGAVEDEDEHATTETMTWATEPDPIVDKPKCCFFSPKIQANRIV	153	
Db	85	RDRVAGESAPEPEPEADYAKETVLMVETHNEIYDKFKQSTHSIYMFNTSELREAV	144	
Qy	154	-----RAQLVHLR---PABEATVFLQISRLMPVKDGGRRHRIKSLKIDVNAVGTWSQ	203	
Db	145	PEPVLSRAELRLRLKLVKQHVLYQKYS-----NNSWYLSNRLLASDSPEWL	197	
Qy	204	SIDVKQVLTVLWKQPTNREIENAY---DAKNDLAV--TSTETGDLGLL-----P	250	
Db	198	SPDVTGVQWLSRGGEIEGFRLSAHCSDSDNTLQVDINGFTTGRGDLATHGNRP	257	
Qy	251	FM-----EVKISEGPKRIIRDSDGLDCE--NSSESCCRYPPLTVDF--EDFGWMIAPKR	302	
Db	258	FLLLMATPLERAQHLOSRHRALDNTNYCFSTKNCVQRLYIDFRKDLGWKWIHPKG	317	
Qy	303	KANYCSGCDYWLQKYPHTH---LVNKASPRGTAGPCCTPTKMSPINLMYFNGKEQII	359	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.2229 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992
Sequence: 1 MHFTQVLISLVLIACGPVG.....KEQIIYKIPSMVVDRCGS 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	3	US-09-841-730-20
2	1992	100.0	374	4	US-10-662-438-8
3	1992	100.0	374	5	US-10-665-374-8
4	1992	100.0	374	5	US-10-991-343-29
5	1989	99.8	374	4	US-10-074-152-36
6	1367.5	68.6	375	3	US-09-454-540-5
7	1367.5	68.6	375	3	US-09-859-211-14
8	1367.5	68.6	375	3	US-09-841-730-2
9	1367.5	68.6	375	3	US-09-872-856-14
10	1367.5	68.6	375	3	US-09-871-604-5
11	1367.5	68.6	375	4	US-10-074-152-29
12	1367.5	68.6	375	4	US-10-278-803-14
13	1367.5	68.6	375	4	US-10-071-499A-1
14	1367.5	68.6	375	4	US-10-335-483-14
15	1367.5	68.6	375	4	US-10-251-115-8
16	1367.5	68.6	375	4	US-10-253-532-130
17	1367.5	68.6	375	4	US-10-365-345-51
18	1367.5	68.6	375	4	US-10-483-973-14
19	1367.5	68.6	375	4	US-10-456-852-4
20	1367.5	68.6	375	4	US-10-459-127-5
21	1367.5	68.6	375	5	US-10-662-438-2
22	1367.5	68.6	375	5	US-10-689-677C-2
23	1367.5	68.6	375	5	US-10-665-374-2
24	1367.5	68.6	375	5	US-10-997-809-14
25	1367.5	68.6	375	5	US-10-991-343-14
26	1367.5	68.6	375	6	US-11-019-001-1
27	1367.5	68.6	376	3	US-09-813-398-38

28	1367.5	68.6	376	5	US-10-826-324-38
29	1363.5	68.4	374	3	US-09-841-730-8
30	1363.5	68.4	375	3	US-09-859-211-23
31	1363.5	68.4	375	3	US-09-872-856-23
32	1363.5	68.4	375	4	US-10-463-973-23
33	1363.5	68.4	375	4	US-10-456-852-10
34	1363.5	68.4	375	4	US-10-662-438-6
35	1363.5	68.4	375	5	US-10-665-374-6
36	1362.5	68.4	375	3	US-09-859-894A-5
37	1360.5	68.3	375	4	US-10-074-152-34
38	1358.5	68.2	375	3	US-09-859-211-27
39	1358.5	68.2	375	3	US-09-841-730-18
40	1358.5	68.2	375	3	US-09-872-856-27
41	1358.5	68.2	375	4	US-10-278-803-19
42	1358.5	68.2	375	4	US-10-463-973-27
43	1358.5	68.2	375	4	US-10-456-852-14
44	1357.5	68.1	375	3	US-09-859-211-19
45	1357.5	68.1	375	3	US-09-859-211-29

ALIGNMENTS

RESULT 1

US-09-841-730-20
; Sequence 20, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Danio rerio
US-09-841-730-20

Query Match 100.0%; Score 1992; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.1e-178; Indels 0; Gaps 0;
Matches 374; Conservative 0; Mismatches 0;

QY	1	MHFTQVLISLVLIACGPVGVDITAHQOPSTATSESLCSTCEFRQHSKMLHAIKQ	60
DB	1	MHFTQVLISLVLIACGPVGVDITAHQOPSTATSESLCSTCEFRQHSKMLHAIKQ	60
QY	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQDLQYDVLGDDSKDGAVEEDEHATTITM	120
DB	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQDLQYDVLGDDSKDGAVEEDEHATTITM	120
QY	121	WTATEPDPVQVDRKPKCCFFSPKIQANRIVRAQLWHLRPAEATTVFLQISRLMPV	180
DB	121	WTATEPDPVQVDRKPKCCFFSPKIQANRIVRAQLWHLRPAEATTVFLQISRLMPV	180
QY	181	KDGRHRIKSLKIDVNAVGTWSQIDVKQVLTVLWKQPTNNGIEINAYDAKNDLAVTS	240
DB	181	KDGRHRIKSLKIDVNAVGTWSQIDVKQVLTVLWKQPTNNGIEINAYDAKNDLAVTS	240
QY	241	TETGEDGLPFFMEVKISEGPKIRRDGDCDSSSESCRCRYPPLTVDFDFGWDIIAP	300
DB	241	TETGEDGLPFFMEVKISEGPKIRRDGDCDSSSESCRCRYPPLTVDFDFGWDIIAP	300

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-20

Perfect score: 1992

Sequence: 1 MHFTQVLISLVLIACGPVG.....KEQIYIGKIPSMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	374	2	US-09-378-238-29
2	1992	100.0	374	2	US-09-626-896-20
3	1992	100.0	374	2	US-09-841-730-20
4	1989	99.8	374	2	US-09-252-149B-36
5	1367.5	68.6	375	1	US-08-525-596B-14
6	1367.5	68.6	375	1	US-08-765-875-5
7	1367.5	68.6	375	2	US-08-795-671-5
8	1367.5	68.6	375	2	US-09-177-860A-14
9	1367.5	68.6	375	2	US-09-252-149B-29
10	1367.5	68.6	375	2	US-09-378-238-14
11	1367.5	68.6	375	2	US-09-451-501-14
12	1367.5	68.6	375	2	US-09-629-938-14
13	1367.5	68.6	375	2	US-09-454-540-5
14	1367.5	68.6	375	2	US-09-686-344-14
15	1367.5	68.6	375	2	US-09-626-896-2
16	1367.5	68.6	375	2	US-09-485-046-4
17	1367.5	68.6	375	2	US-10-278-803-14
18	1367.5	68.6	375	2	US-09-841-730-2
19	1363.5	68.4	374	2	US-09-626-896-8
20	1363.5	68.4	374	2	US-09-841-730-8
21	1363.5	68.4	375	2	US-09-686-344-23
22	1363.5	68.4	375	2	US-09-485-046-10
23	1360.5	68.3	375	2	US-09-252-149B-34
24	1358.5	68.2	375	2	US-09-451-501-19
25	1358.5	68.2	375	2	US-09-686-344-27
26	1358.5	68.2	375	2	US-09-626-896-18
27	1358.5	68.2	375	2	US-09-485-046-14

28	1358.5	68.2	375	2	US-10-278-803-19	Sequence 19, Appl
29	1358.5	68.2	375	2	US-09-841-730-18	Sequence 18, Appl
30	1357.5	68.1	375	2	US-09-252-149B-30	Sequence 30, Appl
31	1357.5	68.1	375	2	US-09-686-344-19	Sequence 19, Appl
32	1357.5	68.1	375	2	US-09-686-344-29	Sequence 29, Appl
33	1357.5	68.1	375	2	US-09-626-896-10	Sequence 10, Appl
34	1357.5	68.1	375	2	US-09-626-896-14	Sequence 14, Appl
35	1357.5	68.1	375	2	US-09-485-046-6	Sequence 6, Appl
36	1357.5	68.1	375	2	US-09-841-730-10	Sequence 10, Appl
37	1357.5	68.1	375	2	US-09-841-730-14	Sequence 14, Appl
38	1355.5	68.0	375	2	US-09-252-149B-35	Sequence 35, Appl
39	1354.5	68.0	375	2	US-09-252-149B-32	Sequence 32, Appl
40	1347.5	67.6	375	2	US-09-451-501-23	Sequence 23, Appl
41	1347.5	67.6	375	2	US-10-278-803-23	Sequence 23, Appl
42	1345.5	67.5	375	2	US-09-686-344-31	Sequence 31, Appl
43	1345.5	67.5	375	2	US-09-626-896-16	Sequence 16, Appl
44	1345.5	67.5	375	2	US-09-841-730-16	Sequence 16, Appl
45	1345.5	67.5	376	1	US-08-525-596B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-378-238-29
; Sequence 29, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JH1120-9
; CURRENT APPLICATION NUMBER: US/09/378,238
; EARLIER FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Danio rerio
US-09-378-238-29

Query Match	100.0%;	Score	1992;	DB	2;	Length	374;
Best Local Similarity	100.0%;	Pred. No.	1.7e-199;				
Matches	374;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	MHFTQVLISLVLIACGPVG	GTAAHQBPSTATESELCTCFRQHSKLMRLHAIK	Q	60		
Db	1	MHFTQVLISLVLIACGPVG	GTAAHQBPSTATESELCTCFRQHSKLMRLHAIK	Q	60		
Qy	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDQYDLGDDSKDGAVEEDEHATTETIM	120				
Db	61	ILSKRLKQAPNISRDVVVKQLLPKAPPLQQLDQYDLGDDSKDGAVEEDEHATTETIM	120				
Qy	121	TMATEPDPIVQVDRKPKCCFFSPKIQANRIVRAQLMWHLRPAEATTVFLQISRLMPV	180				
Db	121	TMATEPDPIVQVDRKPKCCFFSPKIQANRIVRAQLMWHLRPAEATTVFLQISRLMPV	180				
Qy	181	KDGRHRIIRSLKIDVNAVGTISWSQIDVKQVLTWMLKQPETNRGIEINAYDAKGNDLAVTS	240				
Db	181	KDGRHRIIRSLKIDVNAVGTISWSQIDVKQVLTWMLKQPETNRGIEINAYDAKGNDLAVTS	240				
Qy	241	TETGEDLLPFMEVKISGPKRIRRSGLDCDENSESSRCRYPLTVDFDFGWDWIAP	300				

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MQKLAVVYIYLFQILVHP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap:
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap:
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pap:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pap:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	257	12.8	431	1	US-10-816-768-39
3	239	11.9	429	1	US-10-967-457-74
4	236	11.7	364	1	US-10-131-826A-342
5	236	11.7	364	7	US-11-091-334-2
6	234.5	11.6	366	7	US-10-816-768-47
7	228.5	11.3	102	1	US-10-816-768-53
8	221.5	11.0	102	1	US-10-816-768-46
9	219.5	10.9	102	1	US-10-816-768-89
10	219.5	10.9	129	1	US-10-816-768-68
11	219	10.9	139	1	US-10-816-768-100
12	218.5	10.8	203	1	US-10-816-768-69
13	217.5	10.8	117	1	US-10-816-768-85
14	212.5	10.6	102	1	US-10-816-768-86
15	212.5	10.6	102	1	US-10-816-768-55
16	210.5	10.5	102	1	US-10-816-768-56
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.1	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.9	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.7	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KAMUSHIKI KAISHA DPAFORM
; TITLE OF INVENTION: Method for utilizing the 5'end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	26.7%	Pred. No. 9.1e-25;		
Matches	103;	Conservative 57;	Mismatches 131;	Indels 95; Gaps 15;
QY	49	KSRIRPAIKIQLILSKLRLEQAPNISRDVVKQLLPKAPPLQELIDQYDQVQDDSDGSLD	108	
Db	42	KKRIRPAIKIQLILSKLRLEQAPNISRDVVKQLLPKAPPLQELIDQYDQVQDDSDGSLD	95	
QY	109	D-----DYHATTET-IITMPTESDFLVQMEGKPKCCFFKPFSSKIQYNKVKAQLWYL--	160	
Db	96	EPEPEADYAKETVRLVMVETHEI-----YDKPKQSTHSIYMF	135	
QY	161	-----ROVQKPTTVFVQILRLIKPMK-----DGTRYTGIRSLKLDNPNP	199	
Db	136	NTSELREAVPEPVLSSRAELRLRLKLVKEQHVELYQKYNNNSWRYLSNRLAPSDPE	195	
QY	200	TGIWQIDVKTVLQNLKQ-----PESNLGIEIKAFDENGR-DLAVTF	241	
Db	196	---WLSFDVTGVVQWLRSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRDGLATI-	251	
QY	242	PGGEGDLN-PPLEVRVDTFK-----RSRVRDGLDCDEHSTESCCRYPLTVDF-EA	292	
Db	252	-----HGMNRPFLULLMATPLERAHQSSRRALDNTNYCFSTKNCVQQLYIDPKD	306	
QY	293	FGWDWIIAPKRYKANYCSGCEVFLOQYPHPTH---LVHOANPRGSAGPCCTPTKMSPIN	349	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MQKLVYVYILFMQILVHP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2014	100.0	375	3	US-09-859-211-27
2	2014	100.0	375	3	US-09-841-730-18
3	2014	100.0	375	3	US-09-872-856-27
4	2014	100.0	375	4	US-10-463-973-27
5	2014	100.0	375	4	US-10-456-852-14
6	2003	99.5	375	4	US-10-074-152-35
7	1994	99.0	375	3	US-09-859-211-23
8	1994	99.0	375	3	US-09-872-856-23
9	1994	99.0	375	4	US-10-463-973-23
10	1994	99.0	375	4	US-10-456-852-10
11	1994	99.0	375	4	US-10-662-438-6
12	1994	99.0	375	5	US-10-665-374-6
13	1991	98.9	375	4	US-10-074-152-34
14	1989	98.8	374	3	US-09-841-730-8
15	1984	98.5	375	4	US-10-278-803-27
16	1964	97.5	375	4	US-10-278-803-23
17	1871	92.9	375	3	US-09-454-540-5
18	1871	92.9	375	3	US-09-859-211-14
19	1871	92.9	375	3	US-09-841-730-2
20	1871	92.9	375	3	US-08-872-856-14
21	1871	92.9	375	3	US-09-871-604-5
22	1871	92.9	375	4	US-10-074-152-29
23	1871	92.9	375	4	US-10-278-803-14
24	1871	92.9	375	4	US-10-071-499A-1
25	1871	92.9	375	4	US-10-335-483-14
26	1871	92.9	375	4	US-10-251-115-8
27	1871	92.9	375	4	US-10-253-532-130

28	1871	92.9	375	4	US-10-366-345-51	Sequence 51, Appl
29	1871	92.9	375	4	US-10-463-973-14	Sequence 14, Appl
30	1871	92.9	375	4	US-10-456-852-4	Sequence 4, Appl
31	1871	92.9	375	4	US-10-459-127-5	Sequence 5, Appl
32	1871	92.9	375	4	US-10-662-438-2	Sequence 2, Appl
33	1871	92.9	375	5	US-10-689-677C-2	Sequence 2, Appl
34	1871	92.9	375	5	US-10-665-374-2	Sequence 2, Appl
35	1871	92.9	375	5	US-10-997-803-14	Sequence 14, Appl
36	1871	92.9	375	5	US-10-991-343-14	Sequence 14, Appl
37	1871	92.9	375	6	US-11-019-001-1	Sequence 1, Appl
38	1871	92.9	376	5	US-09-813-398-38	Sequence 38, Appl
39	1871	92.9	376	5	US-10-826-324-38	Sequence 38, Appl
40	1866	92.7	375	3	US-09-859-894A-5	Sequence 5, Appl
41	1866	92.7	375	3	US-09-859-211-29	Sequence 29, Appl
42	1866	92.7	375	3	US-09-841-730-14	Sequence 14, Appl
43	1866	92.7	375	3	US-09-872-856-29	Sequence 29, Appl
44	1866	92.7	375	4	US-10-463-973-29	Sequence 29, Appl
45	1863	92.5	375	4	US-10-074-152-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-859-211-27

Query Match	100.0%	Score	2014;	DB	3;	Length	375;
Best Local Similarity	100.0%	Pred	No. 2.4e-181;				
Matches	375;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MQKLVYVYILFMQILVHPVALDGSSQPTENAKDGLNACTWRONTKSSRIEAIKIQI	60				
Db	1	MQKLVYVYILFMQILVHPVALDGSSQPTENAKDGLNACTWRONTKSSRIEAIKIQI	60				
Qy	61	LSKLRLEQAPNISRDIKQLPKAPLOBLIDQYDQDDSSGSLDEDDHYHATTETIIT	120				
Db	61	LSKLRLEQAPNISRDIKQLPKAPLOBLIDQYDQDDSSGSLDEDDHYHATTETIIT	120				
Qy	121	MPTESDPLVQMEGPKCCFFKSSKIQYNKVAQLWIYLRQVKPTTFVQILRLIKPM	180				
Db	121	MPTESDPLVQMEGPKCCFFKSSKIQYNKVAQLWIYLRQVKPTTFVQILRLIKPM	180				
Qy	181	KDQTRYTGIRSLKLDNPNPGTGWISQSDVKTVLQNLWKQPESNIGIEIKAFDENGRLAVT	240				

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-18
Perfect score: 2014
Sequence: 1 MOKLAVYVYILFMQILVHP.....KEQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2014	100.0	375	2	US-09-686-344-27
2	2014	100.0	375	2	US-09-626-896-18
3	2014	100.0	375	2	US-09-485-046-14
4	2014	100.0	375	2	US-09-841-730-18
5	2003	99.5	375	2	US-09-252-149B-35
6	1994	99.0	375	2	US-09-686-344-23
7	1994	99.0	375	2	US-09-485-046-10
8	1991	98.9	375	2	US-09-252-149B-34
9	1989	98.8	374	2	US-09-626-896-8
10	1989	98.8	374	2	US-09-841-730-8
11	1984	98.5	375	2	US-09-451-501-27
12	1984	98.5	375	2	US-10-278-803-27
13	1964	97.5	375	2	US-09-451-501-23
14	1964	97.5	375	2	US-10-278-803-23
15	1871	92.9	375	1	US-08-525-596B-14
16	1871	92.9	375	1	US-08-765-875-5
17	1871	92.9	375	2	US-08-795-671-5
18	1871	92.9	375	2	US-09-177-860A-14
19	1871	92.9	375	2	US-09-252-149B-29
20	1871	92.9	375	2	US-09-378-238-14
21	1871	92.9	375	2	US-09-451-501-14
22	1871	92.9	375	2	US-09-629-938-14
23	1871	92.9	375	2	US-09-454-540-5
24	1871	92.9	375	2	US-09-686-344-14
25	1871	92.9	375	2	US-09-626-896-2
26	1871	92.9	375	2	US-09-485-046-4
27	1871	92.9	375	2	US-10-278-803-14

28	1871	92.9	375	2	US-09-841-730-2	Sequence 2, Appli
29	1866	92.7	375	2	US-09-686-344-29	Sequence 29, Appl
30	1866	92.7	375	2	US-09-626-896-14	Sequence 14, Appl
31	1866	92.7	375	2	US-09-841-730-14	Sequence 14, Appl
32	1863	92.5	375	2	US-09-252-149B-32	Sequence 32, Appl
33	1862	92.5	375	2	US-09-451-501-19	Sequence 19, Appl
34	1862	92.5	375	2	US-10-278-803-19	Sequence 19, Appl
35	1861	92.4	375	2	US-09-252-149B-30	Sequence 30, Appl
36	1861	92.4	375	2	US-09-686-344-19	Sequence 19, Appl
37	1861	92.4	375	2	US-09-626-896-10	Sequence 10, Appl
38	1861	92.4	375	2	US-09-485-046-6	Sequence 6, Appli
39	1861	92.4	375	2	US-09-841-730-10	Sequence 10, Appl
40	1847	91.7	376	1	US-08-525-596B-12	Sequence 12, Appl
41	1847	91.7	376	2	US-09-177-860A-12	Sequence 12, Appl
42	1847	91.7	376	2	US-08-891-789B-6	Sequence 6, Appli
43	1847	91.7	376	2	US-09-252-149B-27	Sequence 27, Appl
44	1847	91.7	376	2	US-09-378-238-12	Sequence 12, Appl
45	1847	91.7	376	2	US-09-451-501-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-686-344-27
; Sequence 27, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-686-344-27

Query Match	100.0%;	Score 2014;	DB 2;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 1.4e-191;		
Matches	375;	Conservative	0;	Mismatches
			0;	Gaps
				Indels
Qy	1	MOKLAVYVYILFMQILVHPVALDSSQPTENAOKGLCNACTWRQNTKSSRIEAIKIQI	60	
Db	1	MOKLAVYVYILFMQILVHPVALDSSQPTENAOKGLCNACTWRQNTKSSRIEAIKIQI	60	
Qy	61	LSKRLKQAPNLSRDVIKOLLKPAPLQELIDQYDQVRDSSDGSLEDDDYHATTETIT	120	
Db	61	LSKRLKQAPNLSRDVIKOLLKPAPLQELIDQYDQVRDSSDGSLEDDDYHATTETIT	120	
Qy	121	MPTESDFLVQMEGKPKCCFFKSSKIQYNKVKQAQMIYLROVQKPTTVFVQILRLIKPM	180	
Db	121	MPTESDFLVQMEGKPKCCFFKSSKIQYNKVKQAQMIYLROVQKPTTVFVQILRLIKPM	180	
Qy	181	KDGTRYTGIRSLKLDNMPGTGIWQSIDVKTVLQNLKOPESNLGIEIKAFDENGRLAVT	240	
Db	181	KDGTRYTGIRSLKLDNMPGTGIWQSIDVKTVLQNLKOPESNLGIEIKAFDENGRLAVT	240	

GenCore version 5.i.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-16

Perfect score: 2011

Sequence: 1 MQKLQIFVYIYLFMLLVAGP.....KEQIYKIGKIFGVVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	260	12.9	431	1	US-10-816-768-39
3	246	12.2	429	1	US-10-967-457-74
4	245.5	12.2	366	7	US-11-091-334-9
5	238.5	11.9	364	1	US-10-131-826A-342
6	238.5	11.9	364	7	US-11-091-334-2
7	230.5	11.5	102	1	US-10-816-768-47
8	223.5	11.1	102	1	US-10-816-768-53
9	222.5	11.1	102	1	US-10-816-768-46
10	221.5	11.0	203	1	US-10-816-768-100
11	220.5	11.0	129	1	US-10-816-768-89
12	220	10.9	139	1	US-10-816-768-68
13	218.5	10.9	117	1	US-10-816-768-69
14	214.5	10.7	102	1	US-10-816-768-55
15	212.5	10.6	102	1	US-10-816-768-85
16	212.5	10.6	102	1	US-10-816-768-86
17	212.5	10.6	102	1	US-10-816-768-88
18	211.5	10.5	102	1	US-10-816-768-84
19	211	10.5	101	1	US-10-816-768-59
20	207.5	10.3	106	1	US-10-816-768-62
21	207.5	10.3	106	1	US-10-816-768-63
22	207	10.3	101	1	US-10-816-768-83
23	206.5	10.3	102	1	US-10-816-768-83
24	205.5	10.2	98	1	US-10-816-768-41
25	205.5	10.2	102	1	US-10-816-768-52

26	205.5	10.2	102	1	US-10-816-768-87	Sequence 87, Appl
27	204.5	10.2	102	1	US-10-816-768-56	Sequence 56, Appl
28	202.5	10.1	98	1	US-10-816-768-42	Sequence 42, Appl
29	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
30	191	9.5	103	1	US-10-816-768-50	Sequence 50, Appl
31	190.5	9.5	98	1	US-10-816-768-44	Sequence 44, Appl
32	189.5	9.4	98	1	US-10-816-768-43	Sequence 43, Appl
33	188.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
34	188	9.3	103	1	US-10-816-768-54	Sequence 54, Appl
35	188	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
36	182.5	9.1	98	1	US-10-816-768-40	Sequence 40, Appl
37	182	9.1	35	1	US-10-816-768-9	Sequence 9, Appl
38	180.5	9.0	98	1	US-10-816-768-64	Sequence 64, Appl
39	178.5	8.9	118	1	US-10-816-768-48	Sequence 48, Appl
40	175.5	8.7	102	1	US-10-816-768-57	Sequence 57, Appl
41	143.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	125.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	112	5.6	39	1	US-10-816-768-115	Sequence 115, App
44	111	5.5	105	1	US-10-816-768-61	Sequence 61, Appl
45	110	5.5	39	1	US-10-816-768-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIXEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5'end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.5%	Score 312.5;	DB 1;	Length 391;
Best Local Similarity	27.6%	Pred. No. 3.1e-24;		
Matches	102;	Conservative 61;	Mismatches 145;	Indels 61; Gaps 15;
Qy	49	KSRRLRAIKIILSKURLETAPNISKDAIRQLLPKAPPLRELIDQYVQDDSDGSLD	108	
Db	42	KRKRIEIRAIQILSKRLASPPSQGE-----VPPGFLPEAVLALYNSTRDRVAGEAEP	95	
Qy	109	D-----DYHTVTTT-VITMTPESTDLAEVQEKPCCKCFKFSKIQHNKV-----VKAOL	156	
Db	96	EPPEADYIYAKVTRVLMVMEHNEIYDKFKQSTHSIYMPFNTSELRAVPEPVLSSREL	155	
Qy	157	WYLRPVKPTPTTVFQILRLIKPMKDGTRYTGIRSLKLDNMNPGTGIWQSIDVKTVLQNL	216	
Db	156	RL-LRLKLKVEHQVELYQ--KYSNNSWRYLSNRLAPS DSP--WLSFDVTGVVRQWL	209	
Qy	217	KQPSNLGHEIKA-----LDENGH-----DLAVTFPEGEGLN-PFLEVKV	257	
Db	210	SRGGEIEGFLSAHSCDSRDNTLQVDINGFTTGRGDLATI-----HGMNRPFLLLMA	263	
Qy	258	TDTTPK-----RSREDFGLDCEHSTESCCRYPLTVDF-EAFGMDWIAPKRYKANYC	309	
Db	264	TLERAQHLOSSHRRALDNTNYCFSTERNCCVQRQYIDPRKDLGKWKWIHEPKGYHANFC	323	
Qy	310	SGCEPFLQKYPHPTH---LVHOANPKGSAGPCCCTPTKMSPINMLYFNKGKQIYIGKIPG	366	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-16
Perfect score: 2011
Sequence: 1 MQLQIFVYIYLFMLLVAGP.....KEQIYKIFGMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2011	100.0	375	3	US-09-859-211-31
2	2011	100.0	375	3	US-09-841-730-16
3	2011	100.0	375	3	US-09-872-856-31
4	2011	100.0	375	4	US-10-463-973-31
5	2008	99.9	375	4	US-10-074-152-33
6	1943	96.6	375	3	US-09-859-211-29
7	1943	96.6	375	3	US-09-841-730-14
8	1943	96.6	375	3	US-09-872-856-29
9	1943	96.6	375	4	US-10-463-973-29
10	1940	96.5	375	4	US-10-074-152-32
11	1917	95.3	375	3	US-09-454-540-5
12	1917	95.3	375	3	US-09-859-211-14
13	1917	95.3	375	3	US-09-841-730-2
14	1917	95.3	375	3	US-09-872-856-14
15	1917	95.3	375	3	US-09-871-604-5
16	1917	95.3	375	4	US-10-074-152-29
17	1917	95.3	375	4	US-10-278-803-14
18	1917	95.3	375	4	US-10-071-499A-1
19	1917	95.3	375	4	US-10-335-483-14
20	1917	95.3	375	4	US-10-251-115-8
21	1917	95.3	375	4	US-10-253-532-130
22	1917	95.3	375	4	US-10-366-345-51
23	1917	95.3	375	4	US-10-463-973-14
24	1917	95.3	375	4	US-10-456-852-4
25	1917	95.3	375	4	US-10-459-137-5
26	1917	95.3	375	4	US-10-662-438-2
27	1917	95.3	375	5	US-10-689-677C-2

28	1917	95.3	375	5	US-10-665-374-2
29	1917	95.3	375	5	US-10-997-809-14
30	1917	95.3	375	5	US-10-991-343-14
31	1917	95.3	375	6	US-11-019-001-1
32	1917	95.3	376	3	US-09-813-398-38
33	1917	95.3	376	5	US-10-826-324-38
34	1916	95.3	375	4	US-10-278-803-19
35	1915	95.2	375	3	US-09-859-211-19
36	1915	95.2	375	3	US-09-841-730-10
37	1915	95.2	375	3	US-09-872-856-19
38	1915	95.2	375	4	US-10-074-152-30
39	1915	95.2	375	4	US-10-463-973-19
40	1915	95.2	375	4	US-10-456-852-6
41	1912	95.1	375	3	US-09-859-894A-5
42	1892	94.1	375	4	US-10-278-803-21
43	1890	94.0	375	3	US-09-859-211-21
44	1890	94.0	375	3	US-09-841-730-12
45	1890	94.0	375	3	US-09-872-856-21

ALIGNMENTS

RESULT 1

US-09-859-211-31
; Sequence 31, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Ovine
US-09-859-211-31

Query Match	100.0%;	Score 2011;	DB 3;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 2.7e-180;	Indels 0;	Gaps 0;
Matches 375;	Conservative 0;	Mismatches 0;		
Qy	1	MQLQIFVYIYLFMLLVAGPVDLNENSEQKENVEKGLCNACLRQNNKSRLEAIKIQI	60	
Db	1	MQLQIFVYIYLFMLLVAGPVDLNENSEQKENVEKGLCNACLRQNNKSRLEAIKIQI	60	
Qy	61	LSKLRLTAPNISKDAIRQLLPKAPURELIDQYDVORDDSSDGLSLEDDDYHVTETVIT	120	
Db	61	LSKLRLTAPNISKDAIRQLLPKAPURELIDQYDVORDDSSDGLSLEDDDYHVTETVIT	120	
Qy	121	MPTESDLLAEVQEKPKCCFPKSSKIOHNVKVAQMIYLRPVKPTPTTVFVQILRLIKPM	180	
Db	121	MPTESDLLAEVQEKPKCCFPKSSKIOHNVKVAQMIYLRPVKPTPTTVFVQILRLIKPM	180	
Qy	181	KDGRYTGIRSLKIDMNPPTGIGWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDIAVTT	240	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-16
Perfect score: 2011
Sequence: 1 MOKLQIFVYLYLMLLVAGP.....KEQIYKIPGMVDRCCS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pap.*
4: /cgn2_6/ptodata/1/1aa/pCTus COMB.pap.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2011	100.0	375	2	US-09-686-344-31
2	2011	100.0	375	2	US-09-626-896-16
3	2011	100.0	375	2	US-09-841-730-16
4	2008	99.9	375	2	US-09-252-149B-33
5	1943	96.6	375	2	US-09-686-344-29
6	1943	96.6	375	2	US-09-626-896-14
7	1943	96.6	375	2	US-09-841-730-14
8	1940	96.5	375	2	US-09-252-149B-32
9	1917	95.3	375	1	US-08-525-596B-14
10	1917	95.3	375	1	US-08-765-875-5
11	1917	95.3	375	2	US-08-795-671-5
12	1917	95.3	375	2	US-09-177-860A-14
13	1917	95.3	375	2	US-09-252-149B-29
14	1917	95.3	375	2	US-09-378-238-14
15	1917	95.3	375	2	US-09-451-501-14
16	1917	95.3	375	2	US-09-629-938-14
17	1917	95.3	375	2	US-09-454-540-5
18	1917	95.3	375	2	US-09-686-344-14
19	1917	95.3	375	2	US-09-626-896-2
20	1917	95.3	375	2	US-09-485-046-4
21	1917	95.3	375	2	US-10-278-803-14
22	1917	95.3	375	2	US-08-841-730-2
23	1916	95.3	375	2	US-09-451-501-19
24	1916	95.3	375	2	US-10-278-803-19
25	1915	95.2	375	2	US-09-252-149B-30
26	1915	95.2	375	2	US-09-686-344-19
27	1915	95.2	375	2	US-09-626-896-10

28	1915	95.2	375	2	US-09-485-046-6	Sequence 6, Appl
29	1915	95.2	375	2	US-09-841-730-10	Sequence 10, Appl
30	1892	94.1	375	2	US-09-451-501-21	Sequence 21, Appl
31	1892	94.1	375	2	US-10-278-803-21	Sequence 21, Appl
32	1890	94.0	375	2	US-08-891-789B-2	Sequence 2, Appl
33	1890	94.0	375	2	US-09-686-344-21	Sequence 12, Appl
34	1890	94.0	375	2	US-09-626-896-12	Sequence 21, Appl
35	1890	94.0	375	2	US-09-485-046-8	Sequence 8, Appl
36	1890	94.0	375	2	US-09-841-730-12	Sequence 12, Appl
37	1890	94.0	376	1	US-08-525-596B-12	Sequence 12, Appl
38	1890	94.0	376	2	US-09-177-860A-12	Sequence 12, Appl
39	1890	94.0	376	2	US-08-891-789B-6	Sequence 6, Appl
40	1890	94.0	376	2	US-09-252-149B-27	Sequence 27, Appl
41	1890	94.0	376	2	US-09-378-238-12	Sequence 12, Appl
42	1890	94.0	376	2	US-09-451-501-12	Sequence 12, Appl
43	1890	94.0	376	2	US-09-629-938-12	Sequence 12, Appl
44	1890	94.0	376	2	US-09-686-344-12	Sequence 12, Appl
45	1890	94.0	376	2	US-09-626-896-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-686-344-31
; Sequence 31, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: FCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Ovine
US-09-686-344-31

Query Match	100.0%	Score	2011	DB	2	Length	375
Best Local Similarity	100.0%	Pred. No.	4.2e-185				
Matches	375	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MOKLQIFVYLYLMLLVAGPVDLNENSEQENVEKGLCNACLRQNNKSRLEAIKIQI	60				
Db	1	MOKLQIFVYLYLMLLVAGPVDLNENSEQENVEKGLCNACLRQNNKSRLEAIKIQI	60				
Qy	61	LSKLRLSTAPNISKDAIRQLLPKAPPLRELIDQYDVQRDSSDGSLEDDDDHYHVTETVIT	120				
Db	61	LSKLRLSTAPNISKDAIRQLLPKAPPLRELIDQYDVQRDSSDGSLEDDDDHYHVTETVIT	120				
Qy	121	MPTESDLAEVQEKPKCCFKFSKIQHNKVKQAQLMIYLAPVKTPTTVFVQILRLKPM	180				
Db	121	MPTESDLAEVQEKPKCCFKFSKIQHNKVKQAQLMIYLAPVKTPTTVFVQILRLKPM	180				
Qy	181	KDGTRYTGIRSLKLDMMNPGTGIWQSIDVKTVLQNLWKQPSNLGIEIKALDENGHLAVT	240				
Db	181	KDGTRYTGIRSLKLDMMNPGTGIWQSIDVKTVLQNLWKQPSNLGIEIKALDENGHLAVT	240				

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-14

Perfect score: 2013

Sequence: 1 MQKLQIVYVYLFMLIVAGS.....KEQIIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PUB.pbp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PUB.pbp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PUB.pbp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PUB.pbp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PUB.pbp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PUB.pbp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PUB.pbp.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match %	Length	ID	Description
1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	236.5	11.7	366	7	US-11-091-334-9
4	233	11.6	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	103	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.1	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.4	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.9	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.7	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.3%	Score 308.5;	DB 1;	Length 391;
Best Local Similarity	26.7%	Pred. No. 2.1e-24;		
Matches	103;	Conservative 57;	Mismatches 131;	Indels 95; Gaps 15;
QY	49	KSRLEAIKIQILSKRLKETAPNISKDAIRQLLPKAPURELIDQYDVORDSDSGLD 108		
DB	42	KKRIETAIRGQILSKRLASPPSQS-----VPPGLPEAVLALYNSTRDRVAGSAEP 95		
QY	109	D-----DYHATTET-IITWPTESDILMQVEGPKCFFKFFSKIOYKNVKAQLWYL-- 160		
DB	96	EPEEADYIAKEVTVLMVETHEI-----YDKFKQSTHSIYMF 135		
QY	161	-----RPVKTPTTVFQVQLRIKPKMK-----DGTRYTGIRSLKLDMPG 199		
DB	136	NTSELREAVPEPVLSSRAELRLRLKLVQEHVELYQKYSNNRYLSNRLAPSDE 195		
QY	200	TGIWQSIVKTVLQVNLKQPSNLGIEIKA-----LDENGH-----DLAVTF 241		
DB	196	---WLSFDVTGVVRQWLSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI- 251		
QY	242	PGPBGDGLN-PELEVKVTDTPK-----RBRDRGLDCDEHSTESRCRYPLTVDF-BA 292		
DB	252	-----HGMNRPFLLMATPLERAQHLQSRHRRALDNTYCFSSSTENQCCVRLYIDFRKD 306		
QY	293	FGWDWIIAPKRYKANYCSGECEFFVLQKYPHTH---LVHQANPRGSAGPCCTTTRKMSPIN 349		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-14
Perfect score: 2013
Sequence: 1 MQLQIYVYIYFLMIVAGP.....KEQIYKIPAMVDRGCS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA_Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	100.0	375	3	US-09-859-211-29 Sequence 29, Appl
2	2013	100.0	375	3	US-09-841-730-14 Sequence 14, Appl
3	2013	100.0	375	3	US-09-872-856-29 Sequence 29, Appl
4	2013	100.0	375	4	US-10-463-973-29 Sequence 29, Appl
5	2010	99.9	375	4	US-10-074-152-32 Sequence 32, Appl
6	1979	98.3	375	3	US-09-454-540-5 Sequence 5, Appl
7	1979	98.3	375	3	US-09-859-211-14 Sequence 14, Appl
8	1979	98.3	375	3	US-09-841-730-2 Sequence 2, Appl
9	1979	98.3	375	3	US-09-872-856-14 Sequence 14, Appl
10	1979	98.3	375	3	US-09-871-604-5 Sequence 5, Appl
11	1979	98.3	375	4	US-10-074-152-29 Sequence 29, Appl
12	1979	98.3	375	4	US-10-278-803-14 Sequence 14, Appl
13	1979	98.3	375	4	US-10-071-499A-1 Sequence 1, Appl
14	1979	98.3	375	4	US-10-335-483-14 Sequence 14, Appl
15	1979	98.3	375	4	US-10-251-115-8 Sequence 8, Appl
16	1979	98.3	375	4	US-10-253-532-130 Sequence 130, App
17	1979	98.3	375	4	US-10-366-345-51 Sequence 51, Appl
18	1979	98.3	375	4	US-10-463-973-14 Sequence 14, Appl
19	1979	98.3	375	4	US-10-456-852-4 Sequence 4, Appl
20	1979	98.3	375	4	US-10-459-127-5 Sequence 5, Appl
21	1979	98.3	375	4	US-10-662-438-2 Sequence 2, Appl
22	1979	98.3	375	5	US-10-689-677C-2 Sequence 2, Appl
23	1979	98.3	375	5	US-10-665-374-2 Sequence 2, Appl
24	1979	98.3	375	5	US-10-397-809-14 Sequence 14, Appl
25	1979	98.3	375	5	US-10-391-343-14 Sequence 14, Appl
26	1979	98.3	375	6	US-11-019-001-1 Sequence 1, Appl
27	1979	98.3	376	3	US-09-813-398-38 Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-29

; Sequence 29, Application US/09859211

; Patent NO. US20020157125A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; FILE REFERENCE: 07265/144001

; CURRENT APPLICATION NUMBER: US/09/859,211

; CURRENT FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 09/019,070

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 08/862,445

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 08/847,910

; PRIOR FILING DATE: 1997-04-28

; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 08/525,596

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: PCT/US94/03019

; PRIOR FILING DATE: 1994-03-18

; PRIOR APPLICATION NUMBER: 08/033,923

; PRIOR FILING DATE: 1993-03-19

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 29

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Porcine

US-09-859-211-29

Query Match 100.0%; Score 2013; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.1e-183;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MQLQIYVYIYFLMIVAGPVDLNENSEKENVEKGLCNACMWRONTKSSRLKAIKQI	60
DB	1	MQLQIYVYIYFLMIVAGPVDLNENSEKENVEKGLCNACMWRONTKSSRLKAIKQI	60
QY	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIDQVDQDDSDGSLDDDDYHATTETIIT	120
DB	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIDQVDQDDSDGSLDDDDYHATTETIIT	120
QY	121	MPTESDLIMQVEGKPKCCFFKFSKIQNKVVKAQLWYLRPVKPTTTFVQILRLKPM	180
DB	121	MPTESDLIMQVEGKPKCCFFKFSKIQNKVVKAQLWYLRPVKPTTTFVQILRLKPM	180
QY	181	KDGRYTGIRSLKLDNPGTGIWQSDIVKTVLQNLKQPESNLGIEIKALDENGHLAVT	240

Sequence 38, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 30, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 4, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 27, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 6, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-14
Perfect score: 2013
Sequence: 1 MOKLQIYVYIYLFMLIVAGP.....KGOIIVGKIPAMVVDRCGCS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	100.0	375	2	US-09-686-344-29
2	2013	100.0	375	2	US-09-626-896-14
3	2013	100.0	375	2	US-09-841-730-14
4	2010	99.9	375	2	US-09-252-1498-32
5	1979	98.3	375	1	US-08-525-5968-14
6	1979	98.3	375	1	US-08-765-875-5
7	1979	98.3	375	2	US-08-795-671-5
8	1979	98.3	375	2	US-09-177-860A-14
9	1979	98.3	375	2	US-09-252-1498-29
10	1979	98.3	375	2	US-09-378-238-14
11	1979	98.3	375	2	US-09-451-501-14
12	1979	98.3	375	2	US-09-629-938-14
13	1979	98.3	375	2	US-09-454-540-5
14	1979	98.3	375	2	US-09-686-344-14
15	1979	98.3	375	2	US-09-626-896-2
16	1979	98.3	375	2	US-09-485-046-4
17	1979	98.3	375	2	US-10-278-803-14
18	1979	98.3	375	2	US-09-841-730-2
19	1978	98.3	375	2	US-09-451-501-19
20	1978	98.3	375	2	US-10-278-803-19
21	1977	98.2	375	2	US-09-252-1498-30
22	1977	98.2	375	2	US-09-686-344-19
23	1977	98.2	375	2	US-09-626-896-10
24	1977	98.2	375	2	US-09-485-046-6
25	1977	98.2	375	2	US-09-841-730-10
26	1956	97.2	376	1	US-08-525-596B-12
27	1956	97.2	376	2	US-09-177-860A-12

28	1956	97.2	376	2	US-08-891-789B-6	Sequence 6, Appl
29	1956	97.2	376	2	US-09-252-149B-27	Sequence 27, Appl
30	1956	97.2	376	2	US-09-378-238-12	Sequence 12, Appl
31	1956	97.2	376	2	US-09-451-501-12	Sequence 12, Appl
32	1956	97.2	376	2	US-09-629-938-12	Sequence 12, Appl
33	1956	97.2	376	2	US-09-686-344-12	Sequence 12, Appl
34	1956	97.2	376	2	US-09-626-896-4	Sequence 4, Appl
35	1956	97.2	376	2	US-09-485-046-2	Sequence 2, Appl
36	1956	97.2	376	2	US-10-278-803-12	Sequence 12, Appl
37	1956	97.2	376	2	US-09-841-730-4	Sequence 4, Appl
38	1943	96.5	375	2	US-09-686-344-31	Sequence 31, Appl
39	1943	96.5	375	2	US-09-626-896-16	Sequence 16, Appl
40	1943	96.5	375	2	US-09-841-730-16	Sequence 16, Appl
41	1940	96.4	375	2	US-09-252-149B-33	Sequence 33, Appl
42	1929	95.8	375	2	US-09-451-501-21	Sequence 21, Appl
43	1929	95.8	375	2	US-10-278-803-21	Sequence 21, Appl
44	1928	95.8	376	2	US-09-252-149B-28	Sequence 28, Appl
45	1928	95.8	376	2	US-09-451-501-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-686-344-29
; Sequence 29, Application US/09686344
; Patent No. 6607884
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/686,344
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-686-344-29

Query Match		100.0%;	Score 2013;	DB 2;	Length 375;
Best Local Similarity		100.0%;	Pred. No. 9.2e-188;		
Matches 375;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MOKLQIYVYIYLFMLIVAGPVDLNSENSEKVENKEGLCNACWNRQNTKSSRLAIIQI	60		
DB	1	MOKLQIYVYIYLFMLIVAGPVDLNSENSEKVENKEGLCNACWNRQNTKSSRLAIIQI	60		
QY	61	LSKRLLETAPNTSKDAIRQLLPKAPPLRELIQYDVQRDDSDGSLEDDDYHATTFTIT	120		
DB	61	LSKRLLETAPNTSKDAIRQLLPKAPPLRELIQYDVQRDDSDGSLEDDDYHATTFTIT	120		
QY	121	MPTSDLLMQVGEKPKCCFFKSSKIQNVKVAQLMWYLRPVKPTTTFVQILRLIKPM	180		
DB	121	MPTSDLLMQVGEKPKCCFFKSSKIQNVKVAQLMWYLRPVKPTTTFVQILRLIKPM	180		
QY	181	KDGTRYTGIRSLKLDWNPQTGIWQSDIVKTVLQNLKQPESNLGIEIKALDENGHDLA	240		
DB	181	KDGTRYTGIRSLKLDWNPQTGIWQSDIVKTVLQNLKQPESNLGIEIKALDENGHDLA	240		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-12
Perfect score: 2003
Sequence: 1 MQLQISVIYILFMLIVAGP.....EGQIYKIPAMVVDROGCS 375

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292.5	14.6	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	248.5	12.4	366	7	US-11-091-334-9
4	239.5	12.0	364	1	US-10-131-826A-342
5	239.5	12.0	364	7	US-11-091-334-2
6	228.5	11.4	102	1	US-10-816-768-47
7	225	11.2	429	1	US-10-967-457-74
8	221.5	11.1	102	1	US-10-816-768-53
9	219.5	11.0	129	1	US-10-816-768-89
10	219	10.9	139	1	US-10-816-768-68
11	218.5	10.9	203	1	US-10-816-768-100
12	217.5	10.9	117	1	US-10-816-768-69
13	216.5	10.8	102	1	US-10-816-768-46
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.5	102	1	US-10-816-768-84
18	209.5	10.5	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	203.5	10.2	102	1	US-10-816-768-52
21	203.5	10.2	102	1	US-10-816-768-56
22	203.5	10.2	102	1	US-10-816-768-83
23	202.5	10.1	102	1	US-10-816-768-87
24	202.5	10.1	106	1	US-10-816-768-62
25	202.5	10.1	106	1	US-10-816-768-63

26	197	9.8	101	1	US-10-816-768-49	Sequence 49, Appl
27	196.5	9.8	98	1	US-10-816-768-42	Sequence 42, Appl
28	194.5	9.7	98	1	US-10-816-768-41	Sequence 41, Appl
29	191.5	9.6	102	1	US-10-816-768-45	Sequence 45, Appl
30	190	9.5	103	1	US-10-816-768-50	Sequence 50, Appl
31	189	9.4	101	1	US-10-816-768-51	Sequence 51, Appl
32	186.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
33	186.5	9.3	98	1	US-10-816-768-44	Sequence 44, Appl
34	184	9.2	107	1	US-10-816-768-58	Sequence 58, Appl
35	181	9.0	103	1	US-10-816-768-54	Sequence 54, Appl
36	176.5	8.8	98	1	US-10-816-768-40	Sequence 40, Appl
37	176.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	174.5	8.7	118	1	US-10-816-768-48	Sequence 48, Appl
39	173.5	8.7	102	1	US-10-816-768-57	Sequence 57, Appl
40	168	8.4	35	1	US-10-816-768-9	Sequence 9, Appl
41	153.5	7.7	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5'end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	14.6%	Score 292.5;	DB 1;	Length 391;
Best Local Similarity	26.4%	Pred. No. 1.9e-23;		
Matches	101;	Conservative	56;	Mismatches 131; Indels 95; Gaps 15;
Qy	52	RLEAKITQILSKURLETAPNISKDAIRQLLPKAPPLLELDIQFPVQDASDGSLEDD--	109	
Db	45	RIEAIRQILSKLRASPPSQGE-----VPPGFLPEAVLALYNSTRDRVAGESAEPEPE	98	
Qy	110	---DYHARTT-VITMPTESDLTQVEGKPKCCFFKSSKIQYNKLVKAQLWYL----	160	
Db	99	PEADYAKVYTRVLVMETHNEI-----YDKFQSTHSIIYFNTS	138	
Qy	161	---RPVKTPATVFQILRLIKPMK-----DGTRYTGIRSLKLDNMPGTGI	202	
Db	139	ELRENPPEFVLLSGASLRLRLKLVQEHVELYQKYSNNRWYLSNRLAPSDE---	195	
Qy	203	WQSIDVKTVLQNLKOPESNLGIEKA-----LDENGH-----DLAVTPEP	244	
Db	196	WLSFDVTGVVRQWLRSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRRGDLATI----	251	
Qy	245	GEGLT-PFLEVKVTTDPK-----RSRDFGLDCDEHSTESCRCYPPLTVDE-EAPGW	295	
Db	252	--HGMNRPFLLMATPLERAQHLQSRHRRALDNTNYCFSSTEKNCCVQQLYIDFRKDLGW	309	
Qy	296	DWIIAPKRYKYNCSGECEFFVLQKYPHPTH---LVHOANPRGSAGPCCTTKMSPINMLY	352	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-12
Perfect score: 2003
Sequence: 1 MQLQISVYIYLFMLIVAGP.....EGQIIYKIPAMVVDRCGCS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA>Main:*
- 1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2003	100.0	375	3	US-09-859-211-21
2	2003	100.0	375	3	US-09-841-730-12
3	2003	100.0	375	3	US-09-872-856-21
4	2003	100.0	375	4	US-10-251-115-2
5	2003	100.0	375	4	US-10-463-973-21
6	2003	100.0	375	4	US-10-456-852-8
7	2003	100.0	375	4	US-10-662-438-4
8	2003	100.0	375	5	US-10-665-374-4
9	2000	99.9	375	4	US-10-074-152-31
10	1997	99.7	375	4	US-10-074-152-2
11	1973	98.5	375	3	US-10-278-803-21
12	1927	96.2	375	3	US-09-859-211-29
13	1927	96.2	375	3	US-09-841-730-14
14	1927	96.2	375	3	US-09-872-856-29
15	1927	96.2	375	4	US-10-463-973-29
16	1924	96.1	375	3	US-10-074-152-32
17	1906	95.2	375	3	US-09-454-540-5
18	1906	95.2	375	3	US-09-859-211-14
19	1906	95.2	375	3	US-09-841-730-2
20	1906	95.2	375	3	US-09-872-856-14
21	1906	95.2	375	3	US-09-871-604-5
22	1906	95.2	375	4	US-10-074-152-29
23	1906	95.2	375	4	US-10-278-803-14
24	1906	95.2	375	4	US-10-071-499A-1
25	1906	95.2	375	4	US-10-335-483-14
26	1906	95.2	375	4	US-10-251-115-8
27	1906	95.2	375	4	US-10-253-532-130

28	1906	95.2	375	4	US-10-366-345-51	Sequence 51, Appl
29	1906	95.2	375	4	US-10-463-973-14	Sequence 14, Appl
30	1906	95.2	375	4	US-10-456-852-4	Sequence 4, Appl
31	1906	95.2	375	4	US-10-459-127-5	Sequence 5, Appl
32	1906	95.2	375	4	US-10-662-438-2	Sequence 2, Appl
33	1906	95.2	375	5	US-10-689-677C-2	Sequence 2, Appl
34	1906	95.2	375	5	US-10-665-374-2	Sequence 2, Appl
35	1906	95.2	375	5	US-10-997-809-14	Sequence 14, Appl
36	1906	95.2	375	5	US-10-991-343-14	Sequence 14, Appl
37	1906	95.2	375	6	US-11-019-001-1	Sequence 1, Appl
38	1906	95.2	376	3	US-09-813-398-38	Sequence 38, Appl
39	1906	95.2	376	5	US-10-826-324-38	Sequence 38, Appl
40	1905	95.1	375	4	US-10-278-803-19	Sequence 19, Appl
41	1904	95.1	375	3	US-09-859-211-19	Sequence 19, Appl
42	1904	95.1	375	3	US-09-841-730-10	Sequence 10, Appl
43	1904	95.1	375	3	US-09-872-856-19	Sequence 19, Appl
44	1904	95.1	375	4	US-10-074-152-30	Sequence 30, Appl
45	1904	95.1	375	4	US-10-463-973-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-859-211-21
; Sequence 21, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bovine
US-09-859-211-21

Query Match	100.0%;	Score 2003;	DB 3;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 1.9e-183;		
Matches	375;	Conservative	0;	Mismatches
			0;	Gaps
				0;
QY	1	MQLQISVYIYLFMLIVAGPVDLNENSSQENVEKGLCNACLRWRENTTSSRLAIKIQI	60	
Db	1	MQLQISVYIYLFMLIVAGPVDLNENSSQENVEKGLCNACLRWRENTTSSRLAIKIQI	60	
QY	61	LSKLELTAPNISKDAIRQLLPKAPLLELDQFDVORDASSDGSLEDDDYHARTETVIT	120	
Db	61	LSKLELTAPNISKDAIRQLLPKAPLLELDQFDVORDASSDGSLEDDDYHARTETVIT	120	
QY	121	MPTESDLITQVEGKPKCCFFKPSKIQYNKLVKAQLMIYLRPVKTPATVFVQILRIKPM	180	
Db	121	MPTESDLITQVEGKPKCCFFKPSKIQYNKLVKAQLMIYLRPVKTPATVFVQILRIKPM	180	
QY	181	KDGTRYTGIRSLKLDMPNFGTIWQSIDVKTVLQNLWKOPESNLGIEIKALDENGHDLATV	240	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-12

Perfect score: 2003

Sequence: 1 MOKLQISVYIYLFMLIVAGP.....EGQIIYKIPAMVVDRCGCS 375

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	100.0	375	2	US-08-891-7898-2
2	2003	100.0	375	2	US-09-686-344-21
3	2003	100.0	375	2	US-09-626-896-12
4	2003	100.0	375	2	US-09-485-046-8
5	2003	100.0	375	2	US-09-841-730-12
6	2000	99.9	375	2	US-09-252-1498-31
7	1997	99.7	375	2	US-09-252-1498-2
8	1973	98.5	375	2	US-09-451-501-21
9	1973	98.5	375	2	US-10-278-803-21
10	1927	96.2	375	2	US-09-686-344-29
11	1927	96.2	375	2	US-09-626-896-14
12	1927	96.2	375	2	US-09-841-730-14
13	1924	96.1	375	2	US-09-252-1498-32
14	1906	95.2	375	1	US-08-525-5968-14
15	1906	95.2	375	1	US-08-765-875-5
16	1906	95.2	375	2	US-08-795-671-5
17	1906	95.2	375	2	US-09-177-860A-14
18	1906	95.2	375	2	US-09-252-1498-29
19	1906	95.2	375	2	US-09-378-238-14
20	1906	95.2	375	2	US-09-451-501-14
21	1906	95.2	375	2	US-09-629-938-14
22	1906	95.2	375	2	US-09-454-540-5
23	1906	95.2	375	2	US-09-686-344-14
24	1906	95.2	375	2	US-09-626-896-2
25	1906	95.2	375	2	US-09-485-046-4
26	1906	95.2	375	2	US-10-278-803-14
27	1906	95.2	375	2	US-09-841-730-2

28	1905	95.1	375	2	US-09-451-501-19	Sequence 19, Appl
29	1905	95.1	375	2	US-10-278-803-19	Sequence 19, Appl
30	1904	95.1	375	2	US-09-252-1498-30	Sequence 30, Appl
31	1904	95.1	375	2	US-09-686-344-19	Sequence 19, Appl
32	1904	95.1	375	2	US-09-626-896-10	Sequence 10, Appl
33	1904	95.1	375	2	US-09-485-046-6	Sequence 6, Appl
34	1904	95.1	375	2	US-09-841-730-10	Sequence 10, Appl
35	1890	94.4	375	2	US-09-686-344-31	Sequence 31, Appl
36	1890	94.4	375	2	US-09-626-896-16	Sequence 16, Appl
37	1890	94.4	375	2	US-09-841-730-16	Sequence 16, Appl
38	1887	94.2	375	2	US-09-252-1498-33	Sequence 33, Appl
39	1876	93.7	376	1	US-08-525-5968-12	Sequence 12, Appl
40	1876	93.7	376	2	US-09-177-860A-12	Sequence 12, Appl
41	1876	93.7	376	2	US-08-891-7898-6	Sequence 6, Appl
42	1876	93.7	376	2	US-09-252-1498-27	Sequence 27, Appl
43	1876	93.7	376	2	US-09-378-238-12	Sequence 12, Appl
44	1876	93.7	376	2	US-09-451-501-12	Sequence 12, Appl
45	1876	93.7	376	2	US-09-629-938-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-08-891-7898-2
; Sequence 2, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Blake, Casels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-891-7898-2

Query Match 100.0%; Score 2003; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOKLQISVYIYLFMLIVAGPVDLNENSEQENVEKGLCNACILWRENTTSSRLAIIKQI 60
Db 1 MOKLQISVYIYLFMLIVAGPVDLNENSEQENVEKGLCNACILWRENTTSSRLAIIKQI 60
QY 61 LSKRLLETAPNISKDAIRQLLPKAPLLELIQDFQVQDASSDGSLEDDDYHARTETVIT 120
Db 61 LSKRLLETAPNISKDAIRQLLPKAPLLELIQDFQVQDASSDGSLEDDDYHARTETVIT 120

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-10
Perfect score: 2016
Sequence: 1 MQLQLCVYIYFLMIVAGP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312.5	15.5	391	1	US-10-517-544-77
2	260	12.9	421	1	US-10-816-768-39
3	242.5	12.0	366	7	US-11-091-334-9
4	236.5	11.7	364	1	US-11-091-334-9
5	236.5	11.7	364	7	US-11-091-334-2
6	234	11.6	429	1	US-10-967-457-74
7	232.5	11.5	102	1	US-10-816-768-47
8	225.5	11.2	102	1	US-10-816-768-53
9	223.5	11.1	129	1	US-10-816-768-89
10	223	11.1	139	1	US-10-816-768-68
11	222.5	11.0	203	1	US-10-816-768-100
12	221.5	11.0	102	1	US-10-816-768-46
13	221.5	11.0	117	1	US-10-816-768-69
14	216.5	10.7	102	1	US-10-816-768-85
15	216.5	10.7	102	1	US-10-816-768-86
16	214.5	10.6	102	1	US-10-816-768-55
17	213.5	10.6	102	1	US-10-816-768-84
18	213.5	10.6	102	1	US-10-816-768-88
19	212	10.5	101	1	US-10-816-768-59
20	208.5	10.3	106	1	US-10-816-768-62
21	208.5	10.3	106	1	US-10-816-768-63
22	207.5	10.3	102	1	US-10-816-768-52
23	207.5	10.3	102	1	US-10-816-768-56
24	206.5	10.2	102	1	US-10-816-768-87
25	206	10.2	101	1	US-10-816-768-49

26 205.5 10.2 102 1 US-10-816-768-83
27 203.5 10.1 98 1 US-10-816-768-41
28 203.5 10.1 98 1 US-10-816-768-42
29 195 9.7 103 1 US-10-816-768-50
30 194 9.6 101 1 US-10-816-768-51
31 193.5 9.6 98 1 US-10-816-768-44
32 192.5 9.5 98 1 US-10-816-768-43
33 192.5 9.5 102 1 US-10-816-768-45
34 189 9.4 107 1 US-10-816-768-58
35 185.5 9.2 98 1 US-10-816-768-40
36 182.5 9.1 98 1 US-10-816-768-64
37 182 9.0 103 1 US-10-816-768-54
38 178.5 8.9 118 1 US-10-816-768-48
39 177.5 8.8 102 1 US-10-816-768-57
40 176 8.7 35 1 US-10-816-768-9
41 146.5 7.3 102 1 US-10-816-768-60
42 124.5 6.2 104 1 US-10-816-768-65
43 113 5.6 105 1 US-10-816-768-61
44 111 5.5 39 1 US-10-816-768-115
45 109 5.4 39 1 US-10-816-768-119

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match 15.5%; Score 312.5; DB 1; Length 391;
Best Local Similarity 27.2%; Pred. No. 3.3e-25;
Matches 105; Conservative 55; Mismatches 131; Indels 95; Gaps 15;
Qy 49 KSRRIEAIKTIQILSKLLETAPNISKDAIRQLLPKAPRLRLDIQYVQRDDSDGSLD 108
Db 42 KRRIEAIKTIQILSKLLETAPNISKDAIRQLLPKAPRLRLDIQYVQRDDSDGSLD 95
Qy 109 D-----DYHATTIT-IITMPTSDFLMQVDPKPKCCFFKSSKIQYNKVKQAQLWYLV-- 160
Db 96 EPSPADYIAKEVTRVLWVETHNEI-----YDKFKOSTHSIYFPP 135
Qy 161 -----RPVETPTTTFVQILRLIKPMK-----DGTTRYTGIRSLKLDNMPG 199
Db 136 NTSLEAREVPEPVLSPALRLRLRLKLVQHVLYQKYSNNRWYLSNRLAPSDSRE 195
Qy 200 TGIWQSIDVKTIVLQNLKQPSNLGIEIKA-----LDENGH-----DLATVF 241
Db 196 ---WLSFDVTGVVQMLSRGGEIEGFRLSAHCSDSRDNTLQVDINGFTTGRGDLATI- 251
Qy 242 PGGEGLN-PELEVKTVDTPK-----RSRRDGLDCDEHSTESCCRYPLTVDF-EA 292
Db 252 -----HGMNRPFLLLMATPLERAHQLQSSRRRALDNTNYCFSTKRCVQLYIDFRKD 306
Qy 293 LGWDWIITAPKRYKANYCGSECFVFLQKYPHTH----LVHOANPRGSGAGCCTPTTNGPIN 349

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-10
Perfect score: 2016
Sequence: 1 MQLQLCVYIYLFMLIVAGP.....KEQIIYKIPAMVVDGCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2016	100.0	375	3	US-09-859-211-19
2	2016	100.0	375	3	US-09-841-730-10
3	2016	100.0	375	3	US-09-872-856-19
4	2016	100.0	375	4	US-10-074-152-30
5	2016	100.0	375	4	US-10-463-973-19
6	2016	100.0	375	4	US-10-456-852-6
7	2008	99.6	375	3	US-09-454-540-5
8	2008	99.6	375	3	US-09-859-211-14
9	2008	99.6	375	3	US-09-841-730-2
10	2008	99.6	375	3	US-09-872-856-14
11	2008	99.6	375	3	US-09-871-604-5
12	2008	99.6	375	4	US-10-074-152-29
13	2008	99.6	375	4	US-10-278-803-14
14	2008	99.6	375	4	US-10-071-499A-1
15	2008	99.6	375	4	US-10-335-483-14
16	2008	99.6	375	4	US-10-251-115-8
17	2008	99.6	375	4	US-10-253-532-130
18	2008	99.6	375	4	US-10-366-345-51
19	2008	99.6	375	4	US-10-463-973-14
20	2008	99.6	375	4	US-10-456-852-4
21	2008	99.6	375	4	US-10-459-127-5
22	2008	99.6	375	4	US-10-662-438-2
23	2008	99.6	375	5	US-10-689-677C-2
24	2008	99.6	375	5	US-10-665-374-2
25	2008	99.6	375	5	US-10-997-809-14
26	2008	99.6	375	5	US-10-991-343-14
27	2008	99.6	375	6	US-11-019-001-1

28	2008	99.6	376	3	US-09-813-398-38	Sequence 38, Appl
29	2008	99.6	376	5	US-10-826-324-38	Sequence 38, Appl
30	2007	99.6	375	4	US-10-378-803-19	Sequence 19, Appl
31	2003	99.4	375	3	US-09-859-894A-5	Sequence 5, Appl
32	1977	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1977	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1977	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1977	98.1	375	4	US-10-463-973-29	Sequence 29, Appl
36	1974	97.9	375	4	US-10-074-152-32	Sequence 32, Appl
37	1951	96.8	376	3	US-09-859-894A-11	Sequence 11, Appl
38	1951	96.8	376	3	US-09-859-211-12	Sequence 12, Appl
39	1951	96.8	376	3	US-09-841-730-4	Sequence 4, Appl
40	1951	96.8	376	3	US-09-872-856-12	Sequence 12, Appl
41	1951	96.8	376	3	US-09-871-604-10	Sequence 10, Appl
42	1951	96.8	376	4	US-10-074-152-27	Sequence 27, Appl
43	1951	96.8	376	4	US-10-378-803-12	Sequence 12, Appl
44	1951	96.8	376	4	US-10-335-483-12	Sequence 12, Appl
45	1951	96.8	376	4	US-10-251-115-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-859-211-19
; Sequence 19, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Baboon
US-09-859-211-19

Query Match		100.0%	Score 2016;	DB 3;	Length 375;
Best Local Similarity		100.0%	Pred. No. 1.1e-182;		
Matches 375;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQLQLCVYIYLFMLIVAGPVDLNSSEKENVKEGLCNACTWRQNTKSSRIEAIKIQI	60		
DB	1	MQLQLCVYIYLFMLIVAGPVDLNSSEKENVKEGLCNACTWRQNTKSSRIEAIKIQI	60		
QY	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIDQYVQRDDSDGSLDDDDYHATTETIIT	120		
DB	61	LSKRLTAPNISKDAIRQLLPKAPPLRELIDQYVQRDDSDGSLDDDDYHATTETIIT	120		
QY	121	MPTSDFLMVDGKPKCCFFKSSKIQYKVKVKAOLWYLRPVETPTTVFVQILRLIKPM	180		
DB	121	MPTSDFLMVDGKPKCCFFKSSKIQYKVKVKAOLWYLRPVETPTTVFVQILRLIKPM	180		
QY	181	KDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPSNLGIEIKALDENGDLAVT	240		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.39627 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-8

Perfect score: 2006

Sequence: 1 OKLAVYVYVLFMQIADPV.....KEQIYGIKIPAMVVDRCGS 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.5	15.7	391	1	US-10-517-544-77
2	255	12.7	431	1	US-10-816-768-39
3	237	11.8	429	1	US-10-967-457-74
4	235	11.7	364	1	US-10-131-826A-342
5	235	11.7	364	7	US-11-091-334-2
6	233.5	11.6	366	7	US-11-091-334-9
7	228.5	11.4	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.9	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.6	102	1	US-10-816-768-85
15	212.5	10.6	102	1	US-10-816-768-86
16	210.5	10.5	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.4	101	1	US-10-816-768-59
20	206.5	10.3	106	1	US-10-816-768-62
21	206.5	10.3	106	1	US-10-816-768-63
22	204	10.2	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.1	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.6	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.5	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.4	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	9.0	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.9	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.8	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.7	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1

US-10-517-544-77

; Sequence 77, Application US/10517544

; Publication NO. US20050250100A1

; GENERAL INFORMATION:

; APPLICANT: RIKEN

; APPLICANT: KABUSHIKI KAISHA DANAFORM

; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis

; FILE REFERENCE: 1336 (PCT)

; CURRENT APPLICATION NUMBER: US/10/517,544

; CURRENT FILING DATE: 2004-12-10

; PRIOR APPLICATION NUMBER: JP 2002-171851

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: JP 2002-235294

; PRIOR FILING DATE: 2002-08-12

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 77

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-517-544-77

Query Match 15.7%; Score 315.5; DB 1; Length 391;

Best Local Similarity 27.1%; Pred. No. 4.6e-25;

Matches 105; Conservative 57; Mismatches 128; Indels 97; Gaps 16;

QY 48 KSRIRBAIKIQLSKURLSQAPNISRDVTKQLPKAPPLQELIDQVDVQDDSDSGSLED 107

Db 42 KRRRIEIRGQILSKURLASPPSQGE-----VPPGPLEAVLALYNSTRDRVAGESAEP 95

QY 108 D-----DYHATTET-IITPTESDPLVQMEGRKCCFFKSSKIQYNKVKAQLWIYL-- 159

Db 96 EPEPEADYIAKEVTRVLMVETHNEI-----YDKFKQSTHSIMWFF 135

QY 160 -----RQVQKPTTFVQILRLIKPMK-----DGTRYTGIRSLKLDNMPG 198

Db 136 NTSELREAVPEPVLSSAEIRLLRLKLVQHQVELYQKYSNNWSWYLSNRLAPSDSPE 195

QY 199 TGMQSIDVKTVLQNLKQ-----PESNLGIEIKAFDGTGR--DLAVT 239

Db 196 ---WLSFDVTGVVRQWLSRGGEIEGFRLSAHCSDSRDNTLQVDINGF-TTGRGDLATI 251

QY 240 FPGCGEDGLN-PFLVRVTDTPK-----RSPRDLDCDEHSTSRCCRYPLTVDF-E 290

Db 252 -----HGMNRPFLLMATPLERAQHLQSSRRHRAIDTNYCFSSSTKNCVCVRLYIDFRK 305

QY 291 AFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTH---LVHQANPRGSAGPCCTPTTKMSPI 347

1	2006	100.0	374	3	US-09-841-730-8	Sequence 8, Appl
2	2006	100.0	375	3	US-09-859-211-23	Sequence 23, Appl
3	2006	100.0	375	3	US-09-872-856-23	Sequence 23, Appl
4	2006	100.0	375	4	US-10-463-973-23	Sequence 23, Appl
5	2006	100.0	375	4	US-10-456-852-10	Sequence 10, Appl
6	2006	100.0	375	4	US-10-462-438-6	Sequence 6, Appl
7	2006	100.0	375	5	US-10-665-374-6	Sequence 6, Appl
8	2003	99.9	375	4	US-10-074-152-34	Sequence 34, Appl
9	1989	99.2	375	3	US-09-859-211-27	Sequence 27, Appl
10	1989	99.2	375	3	US-09-841-730-18	Sequence 18, Appl
11	1989	99.2	375	3	US-09-872-856-27	Sequence 27, Appl
12	1989	99.2	375	4	US-10-463-973-27	Sequence 27, Appl
13	1989	99.2	375	4	US-10-456-852-14	Sequence 14, Appl
14	1978	98.6	375	4	US-10-074-152-35	Sequence 35, Appl
15	1976	98.5	375	4	US-10-278-803-23	Sequence 23, Appl
16	1959	97.7	375	4	US-10-278-803-27	Sequence 27, Appl
17	1860	92.7	375	3	US-09-454-540-5	Sequence 5, Appl
18	1860	92.7	375	3	US-09-859-211-14	Sequence 14, Appl
19	1860	92.7	375	3	US-09-841-730-2	Sequence 2, Appl
20	1860	92.7	375	3	US-09-872-856-14	Sequence 14, Appl
21	1860	92.7	375	3	US-09-871-604-5	Sequence 5, Appl
22	1860	92.7	375	4	US-10-074-152-29	Sequence 29, Appl
23	1860	92.7	375	4	US-10-278-803-14	Sequence 14, Appl
24	1860	92.7	375	4	US-10-071-499A-1	Sequence 1, Appl
25	1860	92.7	375	4	US-10-335-483-14	Sequence 14, Appl
26	1860	92.7	375	4	US-10-251-115-8	Sequence 8, Appl
27	1860	92.7	375	4	US-10-253-533-130	Sequence 130, Appl

Query Match	100.00%;	Score 2006;	DB 3;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 1.3e-180;		
Matches 374;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QKLVVYIYLFQIATAVDPVALDGGSSOPTENAEKGLCNACTWRQNTKSSRIEAIKIQIL	60	
Db	1	QKLVVYIYIYLFQIATAVDPVALDGGSSOPTENAEKGLCNACTWRQNTKSSRIEAIKIQIL	60	
QY	61	SKLRLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSSGCSLEDDDYHATTETIITM	120	
Db	61	SKLRLEQAPNISRDVIKQLLPKAPPLQELIDQYDVQDRDSSGCSLEDDDYHATTETIITM	120	
QY	121	PTSDPFLVMEGKPKCCPFKFSKIQYNKVKVAQLWIYLRQVKQPTTVFVQIILRLIKPMK	180	
Db	121	PTSDPFLVMEGKPKCCPFKFSKIQYNKVKVAQLWIYLRQVKQPTTVFVQIILRLIKPMK	180	
QY	181	DGTRYTGIRSLKLDNMPGGIWIQSDIDKTVLQNLWKQPSNLGIEIKAFDETGRDLAVTF	240	
Db	181	DGTRYTGIRSLKLDNMPGGIWIQSDIDKTVLQNLWKQPSNLGIEIKAFDETGRDLAVTF	240	
QY	241	PGFGEDGLNPFLEVRVTDTPFKSRSDPGLDCEHSTPESCCRYPLTVDFPEAFGMDWIIAP	300	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.2512 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-8
Perfect score: 2006
Sequence: 1 OKLAVYVYILFMQIAVDPV.....KEQIYKIPAMVVDRCGS 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUS-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2006	100.0	374	2	US-09-628-896-8
2	2006	100.0	374	2	US-09-841-730-8
3	2006	100.0	375	2	US-09-686-344-23
4	2006	100.0	375	2	US-09-485-046-10
5	2003	99.9	375	2	US-09-252-149B-34
6	1989	99.2	375	2	US-09-686-344-27
7	1989	99.2	375	2	US-09-626-896-18
8	1989	99.2	375	2	US-09-485-046-14
9	1989	99.2	375	2	US-09-841-730-18
10	1978	98.6	375	2	US-09-252-149B-35
11	1976	98.5	375	2	US-09-451-501-23
12	1976	98.5	375	2	US-10-278-803-27
13	1959	97.7	375	2	US-09-451-501-27
14	1959	97.7	375	2	US-10-278-803-27
15	1860	92.7	375	1	US-08-525-596B-14
16	1860	92.7	375	1	US-08-765-875-5
17	1860	92.7	375	1	US-08-795-671-5
18	1860	92.7	375	2	US-09-177-860A-14
19	1860	92.7	375	2	US-09-252-149B-29
20	1860	92.7	375	2	US-09-378-238-14
21	1860	92.7	375	2	US-09-451-501-14
22	1860	92.7	375	2	US-09-629-938-14
23	1860	92.7	375	2	US-09-454-540-5
24	1860	92.7	375	2	US-09-686-344-14
25	1860	92.7	375	2	US-09-626-896-2
26	1860	92.7	375	2	US-09-485-046-4
27	1860	92.7	375	2	US-10-278-803-14

28	1860	92.7	375	2	US-09-841-730-2
29	1855	92.5	375	2	US-09-686-344-29
30	1855	92.5	375	2	US-09-626-896-14
31	1855	92.5	375	2	US-09-841-730-14
32	1852	92.3	375	2	US-09-252-149B-32
33	1851	92.3	375	2	US-09-451-501-19
34	1851	92.3	375	2	US-10-278-803-19
35	1850	92.2	375	2	US-09-252-149B-30
36	1850	92.2	375	2	US-09-686-344-19
37	1850	92.2	375	2	US-09-626-896-10
38	1850	92.2	375	2	US-09-485-046-6
39	1850	92.2	375	2	US-09-841-730-10
40	1842	91.8	376	1	US-08-525-596B-12
41	1842	91.8	376	2	US-09-177-860A-12
42	1842	91.8	376	2	US-08-891-789B-6
43	1842	91.8	376	2	US-09-252-149B-27
44	1842	91.8	376	2	US-09-378-238-12
45	1842	91.8	376	2	US-09-451-501-12

ALIGNMENTS

RESULT 1
US-09-626-896-8
; Sequence 8, Application US/09626896
; Patent No. 6656475
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/626,896
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-626-896-8

Query Match	100.0%;	Score	2006;	DB 2;	Length	374;			
Best Local Similarity	100.0%;	Pred. No.	8.5e-191;						
Matches	374;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	OKLAVYVYILFMQIAVDPVALDGSQPTENAEKGLCNACTWRONTKSSRIEAIKQIL	60						
Db	1	OKLAVYVYILFMQIAVDPVALDGSQPTENAEKGLCNACTWRONTKSSRIEAIKQIL	60						
Qy	61	SKRLAQAPNISRDVIKQLLPKAPPLQELIDQVQRRDSSDGSLEDDDVHATTETITM	120						
Db	61	SKRLAQAPNISRDVIKQLLPKAPPLQELIDQVQRRDSSDGSLEDDDVHATTETITM	120						
Qy	121	PTSDFLVQMEGPKCCFFKSSKIQNVKVAQLWIYLRQVKPTTVFVQILRLIKPKM	180						
Db	121	PTSDFLVQMEGPKCCFFKSSKIQNVKVAQLWIYLRQVKPTTVFVQILRLIKPKM	180						
Qy	181	DGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLWKQPSNLGEIKAFDSTGRDLAVTF	240						
Db	181	DGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLWKQPSNLGEIKAFDSTGRDLAVTF	240						
Qy	241	PGPEGLNPFLEVRVTDTPKSRRRDGLDCDHSHTESRCRCRYPLTVDFEAFGWDWIAP	300						
Db	241	PGPEGLNPFLEVRVTDTPKSRRRDGLDCDHSHTESRCRCRYPLTVDFEAFGWDWIAP	300						

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-6
Perfect score: 2019
Sequence: 1 MIQKPMVYIYFLVLAAG.....KEIYIKIPAMVDRGCS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	311.5	15.4	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	242	12.0	366	7	US-11-091-334-9
4	236	11.7	429	1	US-10-967-457-74
5	232	11.5	364	1	US-10-131-826A-342
6	232	11.5	364	7	US-11-091-334-2
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.8	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	101	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.4%	Score 311.5;	DB 1;	Length 391;
Best Local Similarity	27.4%	Pred. No. 1.2e-24;		
Matches	105;	Conservative	54;	Mismatches 129;
				Indels 95; Gaps 15;
Qy	53	RIRAIKTIQLSKURLETAPNISKDAIKQLPRAPPLRELIDQYVQRDSDSGSLEDD--	110	
Db	45	RIRAIKTIQLSKURLETAPNISKDAIKQLPRAPPLRELIDQYVQRDSDSGSLEDD--	98	
Qy	111	---DYHATTET-IITMPTESDFLQADGKPKCCFFKSSKIQYKVKVQAQLWIYL----	161	
Db	99	PEADYAKVTRVLMVTHNEI-----YDKFKQSTHSIYWFYTS	138	
Qy	162	---RAVKTPTTVFVQILRLIKPMK-----DCTRYTGIRSLKDMSPGFI	203	
Db	139	ELRAVPEPVLISRAELRLRLKLKVEHQVELYQKYSNNRWYLSNRLAPSDPE---	195	
Qy	204	WQSIDVKTIVLQNWKLQKPSNLGIEKA-----LDENGH-----DLAVTFPGP	245	
Db	196	WLSFDVTGVWRQMLSRGGEIEGFRLSAHSCDSRDNTLQVDINGFTTGRGDLATI----	251	
Qy	246	GEDGLN-PFLEVKYTDTPK-----RSRRDFGLDCDEHSTESRCRYPLTVDF-EAFGW	296	
Db	252	--HGMNRPFLLMATPLERAQHLQSLRRRALDNYCFSTKKNCCVRQLYIDFRKDLGW	309	
Qy	297	DWIIATPKRYKANYCSGCEFFVFLQKYPHTH---LVHQANPRGSAGPCTPTTKMSPINMLY	353	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds
(without-alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-6
Perfect score: 2019
Sequence: 1 MIQKPMYVYLVFLIAG.....KEQIYKIPAMVDRCGS 376

Scoring table: BLASUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2019	100.0	376	3	US-09-859-211-25
2	2019	100.0	376	3	US-09-841-730-6
3	2019	100.0	376	3	US-09-872-856-25
4	2019	100.0	376	4	US-10-074-152-28
5	2019	100.0	376	4	US-10-278-803-25
6	2019	100.0	376	4	US-10-463-973-25
7	2019	100.0	376	4	US-10-456-852-12
8	1986	98.4	376	3	US-09-859-894A-11
9	1986	98.4	376	3	US-09-859-211-12
10	1986	98.4	376	3	US-09-841-730-4
11	1986	98.4	376	3	US-09-872-856-12
12	1986	98.4	376	3	US-09-871-604-10
13	1986	98.4	376	4	US-10-074-152-27
14	1986	98.4	376	4	US-10-278-803-12
15	1986	98.4	376	4	US-10-335-483-12
16	1986	98.4	376	4	US-10-251-115-6
17	1986	98.4	376	4	US-10-463-973-12
18	1986	98.4	376	4	US-10-456-852-2
19	1986	98.4	376	4	US-10-459-127-10
20	1986	98.4	376	5	US-10-997-809-12
21	1986	98.4	376	5	US-10-991-343-12
22	1932	95.7	375	4	US-10-278-803-19
23	1931	95.6	375	4	US-10-074-152-32
24	1928	95.5	375	3	US-09-859-211-29
25	1928	95.5	375	3	US-09-841-730-14
26	1928	95.5	375	3	US-09-872-856-29
27	1928	95.5	375	4	US-10-463-973-29

28	1925	95.3	375	3	US-09-454-540-5	Sequence 5, Appli
29	1925	95.3	375	3	US-09-859-211-14	Sequence 14, Appli
30	1925	95.3	375	3	US-09-841-730-2	Sequence 2, Appli
31	1925	95.3	375	3	US-09-872-856-14	Sequence 14, Appli
32	1925	95.3	375	3	US-09-871-604-5	Sequence 5, Appli
33	1925	95.3	375	4	US-10-074-152-29	Sequence 29, Appli
34	1925	95.3	375	4	US-10-278-803-14	Sequence 14, Appli
35	1925	95.3	375	4	US-10-071-499A-1	Sequence 1, Appli
36	1925	95.3	375	4	US-10-335-483-14	Sequence 14, Appli
37	1925	95.3	375	4	US-10-251-115-8	Sequence 8, Appli
38	1925	95.3	375	4	US-10-253-532-130	Sequence 130, App
39	1925	95.3	375	4	US-10-366-345-51	Sequence 51, Appli
40	1925	95.3	375	4	US-10-463-973-14	Sequence 14, Appli
41	1925	95.3	375	4	US-10-456-852-4	Sequence 4, Appli
42	1925	95.3	375	4	US-10-459-127-5	Sequence 5, Appli
43	1925	95.3	375	4	US-10-662-438-2	Sequence 2, Appli
44	1925	95.3	375	5	US-10-689-677C-2	Sequence 2, Appli
45	1925	95.3	375	5	US-10-665-374-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-859-211-25
; Sequence 25, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-859-211-25

Query Match 100.0%; Score 2019; DB 3; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.1e-186;
Matches 376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MIQKPMYVYLVFLIAGPVLDNEDSREANVEKEGLCNACAWRQNTYRISRIEAIKIQ	60
Db	1	MIQKPMYVYLVFLIAGPVLDNEDSREANVEKEGLCNACAWRQNTYRISRIEAIKIQ	60
Qy	61	ILSKRLTAPNISKDAIRQLPRAPPLRELIQDQVDVQRDSDSGSLEDDEHYATTETII	120
Db	61	ILSKRLTAPNISKDAIRQLPRAPPLRELIQDQVDVQRDSDSGSLEDDEHYATTETII	120
Qy	121	TMPTSDFLMQADGKPKCCFFKFSKIQNKVVKQALWIYLRVKTPTTFVVOILRLIKP	180
Db	121	TMPTSDFLMQADGKPKCCFFKFSKIQNKVVKQALWIYLRVKTPTTFVVOILRLIKP	180
Qy	181	MDGTRYTGIRSLKLDMSFGTQIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHD LAV	240

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-4
Perfect score: 2022
Sequence: 1 MMOKLQWYIYLFMLIAAG.....KEQIYKIPAMVVDRCGS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2022	100.0	376	1	US-08-525-596B-12
2	2022	100.0	376	2	US-09-177-860A-12
3	2022	100.0	376	2	US-08-891-789B-6
4	2022	100.0	376	2	US-09-252-149B-27
5	2022	100.0	376	2	US-09-378-238-12
6	2022	100.0	376	2	US-09-451-501-12
7	2022	100.0	376	2	US-09-629-938-12
8	2022	100.0	376	2	US-09-686-344-12
9	2022	100.0	376	2	US-09-626-896-4
10	2022	100.0	376	2	US-09-485-046-2
11	2022	100.0	376	2	US-10-278-803-12
12	2022	100.0	376	2	US-09-841-730-4
13	1986	98.2	376	2	US-09-252-149B-28
14	1986	98.2	376	2	US-09-451-501-25
15	1986	98.2	376	2	US-09-686-344-25
16	1986	98.2	376	2	US-09-626-896-6
17	1986	98.2	376	2	US-09-485-046-12
18	1986	98.2	376	2	US-10-278-803-25
19	1986	98.2	376	2	US-09-841-730-6
20	1960	96.9	375	2	US-09-451-501-19
21	1960	96.9	375	2	US-10-278-803-19
22	1959	96.9	375	2	US-09-252-149B-32
23	1956	96.7	375	2	US-09-686-344-29
24	1956	96.7	375	2	US-09-626-896-14
25	1956	96.7	375	2	US-09-841-730-14
26	1953	96.6	375	1	US-08-525-596B-14
27	1953	96.6	375	1	US-08-765-875-5

28	1953	96.6	375	2	US-08-795-671-5	Sequence 5, Appl
29	1953	96.6	375	2	US-09-177-860A-14	Sequence 14, Appl
30	1953	96.6	375	2	US-09-252-149B-29	Sequence 29, Appl
31	1953	96.6	375	2	US-09-378-238-14	Sequence 14, Appl
32	1953	96.6	375	2	US-09-451-501-14	Sequence 14, Appl
33	1953	96.6	375	2	US-09-629-938-14	Sequence 14, Appl
34	1953	96.6	375	2	US-09-454-540-5	Sequence 5, Appl
35	1953	96.6	375	2	US-09-686-344-14	Sequence 14, Appl
36	1953	96.6	375	2	US-09-626-896-2	Sequence 2, Appl
37	1953	96.6	375	2	US-09-485-046-4	Sequence 4, Appl
38	1953	96.6	375	2	US-10-278-803-14	Sequence 14, Appl
39	1953	96.6	375	2	US-09-841-730-2	Sequence 2, Appl
40	1951	96.5	375	2	US-09-252-149B-30	Sequence 30, Appl
41	1951	96.5	375	2	US-09-686-344-19	Sequence 19, Appl
42	1951	96.5	375	2	US-09-626-896-10	Sequence 10, Appl
43	1951	96.5	375	2	US-09-485-046-6	Sequence 6, Appl
44	1951	96.5	375	2	US-09-841-730-10	Sequence 10, Appl
45	1893	93.6	375	2	US-09-252-149B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-525-596B-12
; Sequence 12, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P. C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-525-596B-12

Query Match 100.0%; Score 2022; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 7.9e-197; Indels 0; Gaps 0;
Matches 376; Conservative 0; Mismatches 0;
Oy 1 MMOKLQWYIYLFMLIAAGPVDLNEGSEENVEKGLCNACAWRONTRYRTEAIKIQ 60
|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.5771 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-4

Perfect score: 2022

Sequence: 1 MMQKLMYVYIYLFMLIAAG.....KEQIYKIPAMVVDRCGS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2022	100.0	376	3	US-09-859-894A-11
2	2022	100.0	376	3	US-09-859-211-12
3	2022	100.0	376	3	US-09-841-730-4
4	2022	100.0	376	3	US-09-872-856-12
5	2022	100.0	376	3	US-09-871-604-10
6	2022	100.0	376	4	US-10-074-152-27
7	2022	100.0	376	4	US-10-278-803-12
8	2022	100.0	376	4	US-10-335-483-12
9	2022	100.0	376	4	US-10-251-115-6
10	2022	100.0	376	4	US-10-463-973-12
11	2022	100.0	376	4	US-10-456-852-2
12	2022	100.0	376	4	US-10-459-127-10
13	2022	100.0	376	5	US-10-997-809-12
14	2022	100.0	376	5	US-10-991-343-12
15	1986	98.2	376	3	US-09-859-211-25
16	1986	98.2	376	3	US-09-841-730-6
17	1986	98.2	376	3	US-09-872-856-25
18	1986	98.2	376	4	US-10-074-152-28
19	1986	98.2	376	4	US-10-278-803-25
20	1986	98.2	376	4	US-10-463-973-25
21	1986	98.2	376	4	US-10-456-852-12
22	1960	96.9	375	4	US-10-278-803-19
23	1959	96.9	375	4	US-10-074-152-32
24	1956	96.7	375	3	US-09-859-211-29
25	1956	96.7	375	3	US-09-841-730-14
26	1956	96.7	375	3	US-09-872-856-29
27	1956	96.7	375	4	US-10-463-973-29

28	1953	96.6	375	3	US-09-454-540-5	Sequence 5, Appli
29	1953	96.6	375	3	US-09-859-211-14	Sequence 14, Appli
30	1953	96.6	375	3	US-09-841-730-2	Sequence 2, Appli
31	1953	96.6	375	3	US-09-872-856-14	Sequence 14, Appli
32	1953	96.6	375	3	US-09-871-604-5	Sequence 5, Appli
33	1953	96.6	375	4	US-10-074-152-29	Sequence 29, Appli
34	1953	96.6	375	4	US-10-278-803-14	Sequence 14, Appli
35	1953	96.6	375	4	US-10-071-499A-1	Sequence 1, Appli
36	1953	96.6	375	4	US-10-335-483-14	Sequence 8, Appli
37	1953	96.6	375	4	US-10-251-115-8	Sequence 130, App
38	1953	96.6	375	4	US-10-253-532-130	Sequence 51, Appli
39	1953	96.6	375	4	US-10-366-345-51	Sequence 14, Appli
40	1953	96.6	375	4	US-10-463-973-14	Sequence 4, Appli
41	1953	96.6	375	4	US-10-456-852-4	Sequence 5, Appli
42	1953	96.6	375	4	US-10-459-127-5	Sequence 2, Appli
43	1953	96.6	375	4	US-10-662-438-2	Sequence 2, Appli
44	1953	96.6	375	5	US-10-689-677C-2	Sequence 2, Appli
45	1953	96.6	375	5	US-10-665-374-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-859-894A-11
; Sequence 11, Application US/09859894A
; Patent No. US20020150577A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; FILE REFERENCE: JHU1200-9
; CURRENT APPLICATION NUMBER: US/09/859,894A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/019,901
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 08/795,671
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: 08/706,958
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/272,763
; PRIOR FILING DATE: 1994-07-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-859-894A-11

Query Match	100.0%	Score 2022:	DB 3:	Length 376;
Best Local Similarity	100.0%	Pred. No. 2.4e-188;	Indels	0;
Matches	376;	Conservative	0;	Mismatches
Qy	1	MMQKLMYVYIYLFMLIAAGPVDLNEGSEENVEKEGLCNACAWRQNTYRSIEAIKIQ	60	
Db	1	MMQKLMYVYIYLFMLIAAGPVDLNEGSEENVEKEGLCNACAWRQNTYRSIEAIKIQ	60	
Qy	61	ILSKRLLETAPNTSKDAIRQLPAPPLRELIDQYDQVQRDDSDGSLDDDYHATTETII	120	
Db	61	ILSKRLLETAPNTSKDAIRQLPAPPLRELIDQYDQVQRDDSDGSLDDDYHATTETII	120	
Qy	121	TMTESDFLMOADGKPKCCFFKSSKIYKNVKAQLMIYLRPVKTTTTFVQLRLIKP	180	
Db	121	TMTESDFLMOADGKPKCCFFKSSKIYKNVKAQLMIYLRPVKTTTTFVQLRLIKP	180	
Qy	181	MDGTRYTGIRSKLDMSPGTGIWQSIDVKTVLQNWMLKQESNLGIEIKALDENGHDVAV	240	
Db	181	MDGTRYTGIRSKLDMSPGTGIWQSIDVKTVLQNWMLKQESNLGIEIKALDENGHDVAV	240	
Qy	241	TFPGQEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCRCRYPLTVDFEAFGWDWII	300	
Db	241	TFPGQEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCRCRYPLTVDFEAFGWDWII	300	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.40373 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-4
Perfect score: 2022
Sequence: 1 MMQKLMVYVYLFMLIAG.....KEIYIGKIPAMVDRCGS 376

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New.*
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	306.5	15.2	391	1	US-10-517-544-77	Sequence 77, Appl
2	256	12.7	431	1	US-10-816-768-39	Sequence 39, Appl
3	249	12.3	366	7	US-11-091-334-9	Sequence 9, Appl
4	236	11.7	429	1	US-10-967-457-74	Sequence 74, Appl
5	232	11.5	364	1	US-10-131-826A-342	Sequence 342, App
6	232	11.5	364	7	US-11-091-334-2	Sequence 2, Appl
7	228.5	11.3	102	1	US-10-816-768-47	Sequence 47, Appl
8	221.5	11.0	102	1	US-10-816-768-53	Sequence 53, Appl
9	219.5	10.9	102	1	US-10-816-768-46	Sequence 46, Appl
10	219.5	10.9	129	1	US-10-816-768-89	Sequence 89, Appl
11	219	10.8	139	1	US-10-816-768-68	Sequence 68, Appl
12	218.5	10.8	203	1	US-10-816-768-100	Sequence 100, App
13	217.5	10.8	117	1	US-10-816-768-69	Sequence 69, Appl
14	212.5	10.5	102	1	US-10-816-768-85	Sequence 85, Appl
15	212.5	10.5	102	1	US-10-816-768-86	Sequence 86, Appl
16	210.5	10.4	102	1	US-10-816-768-55	Sequence 55, Appl
17	209.5	10.4	102	1	US-10-816-768-84	Sequence 84, Appl
18	209.5	10.4	102	1	US-10-816-768-88	Sequence 88, Appl
19	208	10.3	101	1	US-10-816-768-59	Sequence 59, Appl
20	206.5	10.2	106	1	US-10-816-768-62	Sequence 62, Appl
21	206.5	10.2	106	1	US-10-816-768-63	Sequence 63, Appl
22	204	10.1	101	1	US-10-816-768-49	Sequence 49, Appl
23	203.5	10.1	102	1	US-10-816-768-52	Sequence 52, Appl
24	203.5	10.1	102	1	US-10-816-768-56	Sequence 56, Appl
25	203.5	10.1	102	1	US-10-816-768-83	Sequence 83, Appl

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.5	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 43, Appl
34	187	9.2	107	1	US-10-816-768-58	Sequence 58, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 40, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 54, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 64, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 9, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 48, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 57, Appl
41	142.5	7.0	102	1	US-10-816-768-60	Sequence 60, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 65, Appl
43	111	5.5	39	1	US-10-816-768-115	Sequence 115, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 119, App
45	109	5.4	39	1	US-10-816-768-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KASUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.2%	Score 306.5;	DB 1;	Length 391;
Best Local Similarity	28.1%	Pred. No. 3.1e-24;		
Matches	103;	Conservative 56;	Mismatches 146;	Indels 61; Gaps 14;
Qy	53	RIRAIKIQILSKLRTAPNISDAIRQLLPRAPLRELIDQYDVRDSDSGSLEDD--	110	
Db	45	RIRAIKIQILSKLRTAPNISDAIRQLLPRAPLRELIDQYDVRDSDSGSLEDD--	110	
Qy	111	---DYHATTETIITPTESDFLMOADGKPKCCFKSSKIQYNKW-----KAQLWY 160		
Db	99	PEADYAKVTRVLMVETHNEIYDKPKQSTHSIYFFNTSELREAVPEPVLSSRAELRL- 157		
Qy	161	LRPVKPTPTTVFQILRLIKPMKOGTRVTGTRSLKLDSPGIGIWSIDKVTVLQNLWKQP 220		
Db	158	LRRLKLVKEQVELYQ--KYSNNRWYLSNRLAPSDSPE---WLSFDVTGVVRQWLSRG 212		
Qy	221	ESNLIGIKA-----LDENGH-----DLAVTFPGPGEDGLN-PFLVKVYDT 261		
Db	213	GEIEGFLSLAHCSDSRDNTLQVDINGFTTGRGRLATI-----HGNRRFLLMATPL 266		
Qy	262	PK-----RSRRDFGLDCDEHSTESCCRYPLTVDF-EAFGMDWIIAPKRYKANYCSGE 313		
Db	267	BRAGHLOSSRRRALDNTNYCFSTKCKCCVRLQYIDFRKDLGWKWIHEPKGYHANFCLGP 326		
Qy	314	CEVFLQKYPHTH---LVHQANPRGSAGPCTPTFMGSPINMLYFNGKEIYIGKIPAMV 370		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:18:23 ; Search time 1.4 Seconds
(without alignments)
302.622 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MQLQLCVYIYFLMIVAGP.....KEQIYKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- Published Applications AA New:*
- 1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.5	15.3	391	1	US-10-517-544-77
2	256	12.7	431	1	US-10-816-768-39
3	238.5	11.8	366	7	US-11-091-334-9
4	232	11.5	364	1	US-10-131-826A-342
5	232	11.5	364	7	US-11-091-334-2
6	231	11.4	429	1	US-10-967-457-74
7	228.5	11.3	102	1	US-10-816-768-47
8	221.5	11.0	102	1	US-10-816-768-53
9	219.5	10.9	102	1	US-10-816-768-46
10	219.5	10.9	129	1	US-10-816-768-89
11	219	10.9	139	1	US-10-816-768-68
12	218.5	10.8	203	1	US-10-816-768-100
13	217.5	10.8	117	1	US-10-816-768-69
14	212.5	10.5	102	1	US-10-816-768-85
15	212.5	10.5	102	1	US-10-816-768-86
16	210.5	10.4	102	1	US-10-816-768-55
17	209.5	10.4	102	1	US-10-816-768-84
18	209.5	10.4	102	1	US-10-816-768-88
19	208	10.3	101	1	US-10-816-768-59
20	206.5	10.2	106	1	US-10-816-768-62
21	206.5	10.2	106	1	US-10-816-768-63
22	204	10.1	101	1	US-10-816-768-49
23	203.5	10.1	102	1	US-10-816-768-52
24	203.5	10.1	102	1	US-10-816-768-56
25	203.5	10.1	102	1	US-10-816-768-83

26	202.5	10.0	102	1	US-10-816-768-87	Sequence 87, Appl
27	199.5	9.9	98	1	US-10-816-768-41	Sequence 41, Appl
28	199.5	9.9	98	1	US-10-816-768-42	Sequence 42, Appl
29	193	9.6	103	1	US-10-816-768-50	Sequence 50, Appl
30	192	9.5	101	1	US-10-816-768-51	Sequence 51, Appl
31	190.5	9.4	102	1	US-10-816-768-45	Sequence 45, Appl
32	189.5	9.4	98	1	US-10-816-768-44	Sequence 44, Appl
33	188.5	9.3	98	1	US-10-816-768-43	Sequence 58, Appl
34	187	9.3	107	1	US-10-816-768-58	Sequence 40, Appl
35	181.5	9.0	98	1	US-10-816-768-40	Sequence 54, Appl
36	180	8.9	103	1	US-10-816-768-54	Sequence 64, Appl
37	178.5	8.8	98	1	US-10-816-768-64	Sequence 9, Appl
38	176	8.7	35	1	US-10-816-768-9	Sequence 48, Appl
39	174.5	8.6	118	1	US-10-816-768-48	Sequence 57, Appl
40	173.5	8.6	102	1	US-10-816-768-57	Sequence 60, Appl
41	142.5	7.1	102	1	US-10-816-768-60	Sequence 65, Appl
42	124.5	6.2	104	1	US-10-816-768-65	Sequence 115, App
43	111	5.5	39	1	US-10-816-768-115	Sequence 119, App
44	109	5.4	39	1	US-10-816-768-119	Sequence 120, App
45	109	5.4	39	1	US-10-816-768-120	

ALIGNMENTS

RESULT 1

US-10-517-544-77
; Sequence 77, Application US/10517544
; Publication No. US20050250100A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; APPLICANT: KABUSHIKI KAISHA DNAFORM
; TITLE OF INVENTION: Method for utilizing the 5' end of mRNA for cloning and analysis
; FILE REFERENCE: 1336(PCT)
; CURRENT APPLICATION NUMBER: US/10/517,544
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: JP 2002-171851
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: JP 2002-235294
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-544-77

Query Match	15.3%	Score 308.5;	DB 1;	Length 391;
Best Local Similarity	26.9%	Pred. No. 1.7e-24;		
Matches	104;	Conservative	55;	Mismatches 132; Indels 95; Gaps 15;
Qy	49	KSRRIEAIKTIQLSKRLKLETAIPNISKDVIRQLPAPRLRLIDQVQRDSDSGSLD	108	
Db	42	KRRIEAIKTIQLSKRLKLETAIPNISKDVIRQLPAPRLRLIDQVQRDSDSGSLD	95	
Qy	109	D-----DYHATTET-IITMPTSDFLMQVDPKPCFKSSKIYKVKVQAQLWIYL--	160	
Db	96	EPEEADYAKETVRLMVTHEI-----YDKFKSTHSIYWF	135	
Qy	161	-----RPVETPTTFVQILRLIKPMK-----DGRYTYGIRSLKLDMPG	199	
Db	136	NTSELREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNNRWYLSNLLAPSDSPE	195	
Qy	200	TGIWQSIDVTYVQLNWLKQPNLSLGIKA-----LDENGH-----DLAVTF	241	
Db	196	---WLSFDVTGTVKRWQLSRGGEIEGFLSAHSCDSRDNTLQVDINGFTTGRGDLAT-	251	
Qy	242	PGGEDGLN-PFLVKYVTDTPK-----RSRRDGLDCDEHSTESCCRYPLTVDF--	292	
Db	252	-----HGMNRPFLMLMATPLERAQHLQSSRRRLDNTNYCFSTKRCVQLYIDFRKD	306	
Qy	293	FGDWIITAPKRYKANYCSGCECFVFLQKYPHTH----LVHQANPRGSAGPCCCTPTKMSPIN	349	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:13:27 ; Search time 66.4 Seconds
(without alignments)
2359.729 Million cell updates/sec

Title: US-09-628-112-2

Perfect score: 2018

Sequence: 1 MQLQLCVIYLFMLIVAP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	375	3	US-09-454-540-5
2	2018	100.0	375	3	US-09-859-211-14
3	2018	100.0	375	3	US-09-841-730-2
4	2018	100.0	375	3	US-09-872-856-14
5	2018	100.0	375	3	US-09-871-604-5
6	2018	100.0	375	4	US-10-074-152-29
7	2018	100.0	375	4	US-10-278-803-14
8	2018	100.0	375	4	US-10-071-499A-1
9	2018	100.0	375	4	US-10-335-483-14
10	2018	100.0	375	4	US-10-251-115-8
11	2018	100.0	375	4	US-10-253-532-130
12	2018	100.0	375	4	US-10-368-345-51
13	2018	100.0	375	4	US-10-463-973-14
14	2018	100.0	375	4	US-10-456-852-4
15	2018	100.0	375	4	US-10-459-127-5
16	2018	100.0	375	4	US-10-662-438-2
17	2018	100.0	375	5	US-10-689-677C-2
18	2018	100.0	375	5	US-10-665-374-2
19	2018	100.0	375	5	US-10-997-809-14
20	2018	100.0	375	5	US-10-991-343-14
21	2018	100.0	375	6	US-11-019-001-1
22	2018	100.0	376	3	US-09-813-398-38
23	2018	100.0	376	5	US-10-826-324-38
24	2013	99.8	375	3	US-09-859-894A-5
25	2009	99.6	375	4	US-10-278-803-19
26	2008	99.5	375	3	US-09-859-211-19
27	2008	99.5	375	3	US-09-841-730-10

28	2008	99.5	375	3	US-09-872-856-19	Sequence 19, Appl
29	2008	99.5	375	4	US-10-074-152-30	Sequence 30, Appl
30	2008	99.5	375	4	US-10-463-973-19	Sequence 19, Appl
31	2008	99.5	375	4	US-10-456-852-6	Sequence 6, Appl
32	1979	98.1	375	3	US-09-859-211-29	Sequence 29, Appl
33	1979	98.1	375	3	US-09-841-730-14	Sequence 14, Appl
34	1979	98.1	375	3	US-09-872-856-29	Sequence 29, Appl
35	1979	98.1	375	4	US-10-463-973-23	Sequence 32, Appl
36	1976	97.9	375	4	US-10-074-152-32	Sequence 11, Appl
37	1953	96.8	376	3	US-09-859-894A-11	Sequence 12, Appl
38	1953	96.8	376	3	US-09-859-211-12	Sequence 4, Appl
39	1953	96.8	376	3	US-09-841-730-4	Sequence 12, Appl
40	1953	96.8	376	3	US-09-872-856-12	Sequence 10, Appl
41	1953	96.8	376	3	US-09-871-604-10	Sequence 27, Appl
42	1953	96.8	376	4	US-10-074-152-27	Sequence 12, Appl
43	1953	96.8	376	4	US-10-335-483-12	Sequence 6, Appl
44	1953	96.8	376	4	US-10-251-115-6	
45	1953	96.8	376	4	US-10-251-115-6	

ALIGNMENTS

RESULT 1
US-09-454-540-5
; Sequence 5, Application US/09454540
; Patent No. US20010053358A1
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,540
; FILING DATE: 06-DEC-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILLE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..375
US-09-454-540-5
Query Match 100.0%; Score 2018; DB 3; Length 375;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-2
Perfect score: 2018
Sequence: 1 MQKLQCLVYILFMLIVAGP.....KEQIYKIPAMVVDRCGS 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	375	1	US-08-525-596B-14
2	2018	100.0	375	1	US-08-765-875-5
3	2018	100.0	375	2	US-08-795-671-5
4	2018	100.0	375	2	US-09-177-860A-14
5	2018	100.0	375	2	US-09-252-149B-29
6	2018	100.0	375	2	US-09-378-238-14
7	2018	100.0	375	2	US-09-451-501-14
8	2018	100.0	375	2	US-09-629-938-14
9	2018	100.0	375	2	US-09-454-540-5
10	2018	100.0	375	2	US-09-686-344-14
11	2018	100.0	375	2	US-09-626-896-2
12	2018	100.0	375	2	US-09-485-046-4
13	2018	100.0	375	2	US-10-278-803-14
14	2018	100.0	375	2	US-09-841-730-2
15	2009	99.6	375	2	US-09-451-501-19
16	2009	99.6	375	2	US-10-278-803-19
17	2008	99.5	375	2	US-09-252-149B-30
18	2008	99.5	375	2	US-09-686-344-19
19	2008	99.5	375	2	US-09-626-896-10
20	2008	99.5	375	2	US-09-485-046-6
21	2008	99.5	375	2	US-09-841-730-10
22	1979	98.1	375	2	US-09-686-344-29
23	1979	98.1	375	2	US-09-626-896-14
24	1979	98.1	375	2	US-09-841-730-14
25	1976	97.9	375	2	US-09-252-149B-32
26	1953	96.8	376	1	US-08-525-596B-12
27	1953	96.8	376	2	US-09-177-860A-12

28	1953	96.8	376	2	US-08-891-789B-6	Sequence 6, Appli
29	1953	96.8	376	2	US-09-252-149B-27	Sequence 27, Appli
30	1953	96.8	376	2	US-09-378-238-12	Sequence 12, Appli
31	1953	96.8	376	2	US-09-451-501-12	Sequence 12, Appli
32	1953	96.8	376	2	US-09-629-938-12	Sequence 12, Appli
33	1953	96.8	376	2	US-09-686-344-12	Sequence 12, Appli
34	1953	96.8	376	2	US-09-626-896-4	Sequence 4, Appli
35	1953	96.8	376	2	US-09-485-046-2	Sequence 2, Appli
36	1953	96.8	376	2	US-10-278-803-12	Sequence 12, Appli
37	1953	96.8	376	2	US-09-841-730-4	Sequence 4, Appli
38	1925	95.4	376	2	US-09-252-149B-28	Sequence 28, Appli
39	1925	95.4	376	2	US-09-451-501-25	Sequence 25, Appli
40	1925	95.4	376	2	US-09-686-344-25	Sequence 25, Appli
41	1925	95.4	376	2	US-09-626-896-6	Sequence 6, Appli
42	1925	95.4	376	2	US-09-485-046-12	Sequence 12, Appli
43	1925	95.4	376	2	US-10-278-803-25	Sequence 25, Appli
44	1925	95.4	376	2	US-09-841-730-6	Sequence 6, Appli
45	1917	95.0	375	2	US-09-686-344-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1
US-08-525-596B-14
; Sequence 14, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-525-596B-14

Query Match 100.0%; Score 2018; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQKLQCLVYILFMLIVAGPVDLNSSEQKVENKEGLCNACTWRQTKSRLEAIKIQI 60
|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 ; Search time 18.3488 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-6

Perfect score: 2019

Sequence: 1 MIQKPMVYIYLFVLIAG.....KEIYKIPAMVDRCCS 376

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pap.*
 - 2: /cgn2_6/ptodata/1/1aa/6 COMB.pap.*
 - 3: /cgn2_6/ptodata/1/1aa/H COMB.pap.*
 - 4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pap.*
 - 5: /cgn2_6/ptodata/1/1aa/RE COMB.pap.*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2019	100.0	376	2	US-09-252-149B-28
2	2019	100.0	376	2	US-09-451-501-25
3	2019	100.0	376	2	US-09-686-344-25
4	2019	100.0	376	2	US-09-626-896-6
5	2019	100.0	376	2	US-09-485-046-12
6	2019	100.0	376	2	US-10-278-803-25
7	2019	100.0	376	2	US-09-841-730-6
8	1986	98.4	376	1	US-08-525-596B-12
9	1986	98.4	376	2	US-09-177-860A-12
10	1986	98.4	376	2	US-08-891-789B-6
11	1986	98.4	376	2	US-09-252-149B-27
12	1986	98.4	376	2	US-09-378-238-12
13	1986	98.4	376	2	US-09-451-501-12
14	1986	98.4	376	2	US-09-629-938-12
15	1986	98.4	376	2	US-09-686-344-12
16	1986	98.4	376	2	US-09-626-896-4
17	1986	98.4	376	2	US-09-485-046-2
18	1986	98.4	376	2	US-10-278-803-12
19	1986	98.4	376	2	US-09-841-730-4
20	1932	95.7	375	2	US-09-451-501-19
21	1932	95.7	375	2	US-10-278-803-19
22	1931	95.6	375	2	US-09-252-149B-32
23	1928	95.5	375	2	US-09-686-344-29
24	1928	95.5	375	2	US-09-626-896-14
25	1928	95.5	375	2	US-09-841-730-14
26	1925	95.3	375	1	US-08-525-596B-14
27	1925	95.3	375	1	US-08-765-875-5

ALIGNMENTS

RESULT 1

US-09-252-149B-28
; Sequence 28, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-252-149B-28

Query Match	100.0%	Score 2019;	DB 2;	Length 376;
Best Local Similarity	100.0%	Pred. No. 6.4e-198;		
Matches	376;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	1	MIQKPMVYIYLFVLIAGFVLDNEDSREANVEKEGLCNACAWRONTRYSRIBAIKIQ	60	
Db	1	MIQKPMVYIYLFVLIAGFVLDNEDSREANVEKEGLCNACAWRONTRYSRIBAIKIQ	60	
Oy	61	ILSKRLTAPNISKDAIRQLPRAPPLRELIQDYVQDRDSDSGSLEDDHYATETII	120	
Db	61	ILSKRLTAPNISKDAIRQLPRAPPLRELIQDYVQDRDSDSGSLEDDHYATETII	120	
Oy	121	TMPTESFLMQADGPKCCPKSSKIQYNNKVAQWILYRAVKTPPTVFQIURLIKP	180	
Db	121	TMPTESFLMQADGPKCCPKSSKIQYNNKVAQWILYRAVKTPPTVFQIURLIKP	180	
Oy	181	MKDQTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPSNLGIEIKALDENGHDLA	240	
Db	181	MKDQTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPSNLGIEIKALDENGHDLA	240	
Oy	241	TFPGGEGDLNPFLEVKVTDTPKSRDPLGDCDEHSTESCCRYPLTVDFEAGWDWII	300	
Db	241	TFPGGEGDLNPFLEVKVTDTPKSRDPLGDCDEHSTESCCRYPLTVDFEAGWDWII	300	
Oy	301	APKRYKANCSEGECEVFLOKYPHTHLVHQNPRGSAGPCCTPTKMSPINMLYNGKEQI	360	
Db	301	APKRYKANCSEGECEVFLOKYPHTHLVHQNPRGSAGPCCTPTKMSPINMLYNGKEQI	360	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2005, 17:10:37 : Search time 18.3 Seconds
(without alignments)
1694.174 Million cell updates/sec

Title: US-09-628-112-10

Perfect score: 2016

Sequence: 1 MQKLQCVYIYLFMLIVAGP.....KEQIYIGKIPAMVDRGCS 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5 COMB pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2016	100.0	375	2	US-09-252-149B-30
2	2016	100.0	375	2	US-09-686-344-19
3	2016	100.0	375	2	US-09-628-896-10
4	2016	100.0	375	2	US-09-485-046-6
5	2016	100.0	375	2	US-09-841-730-10
6	2008	99.6	375	1	US-08-525-596B-14
7	2008	99.6	375	1	US-08-765-875-5
8	2008	99.6	375	2	US-08-795-671-5
9	2008	99.6	375	2	US-09-177-860A-14
10	2008	99.6	375	2	US-09-252-149B-29
11	2008	99.6	375	2	US-09-378-238-14
12	2008	99.6	375	2	US-09-451-501-14
13	2008	99.6	375	2	US-09-629-938-14
14	2008	99.6	375	2	US-09-454-540-5
15	2008	99.6	375	2	US-09-686-344-14
16	2008	99.6	375	2	US-09-626-896-2
17	2008	99.6	375	2	US-09-485-046-4
18	2008	99.6	375	2	US-10-278-803-14
19	2008	99.6	375	2	US-09-841-730-2
20	2007	99.6	375	2	US-09-451-501-19
21	2007	99.6	375	2	US-10-278-803-19
22	1977	98.1	375	2	US-09-686-344-29
23	1977	98.1	375	2	US-09-626-896-14
24	1977	98.1	375	2	US-09-841-730-14
25	1974	97.9	375	2	US-09-252-149B-32
26	1951	96.8	376	1	US-08-525-596B-12
27	1951	96.8	376	2	US-09-177-860A-12

RESULT 1
US-09-252-149B-30
; Sequence 30, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; TITLE OF INVENTION: VERTEBRATE SUBJECTS
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Papio hamadryas
US-09-252-149B-30

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB 2;	Length	375;
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MQKLQCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSRIBAIKIQI	60		
Db	1	MQKLQCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSRIBAIKIQI	60		
Qy	61	LSKRLLETAPNISKDAIRQLPKAPRLRELIQYDQVDRDDSDGSLDDDDVHATTEIIT	120		
Db	61	LSKRLLETAPNISKDAIRQLPKAPRLRELIQYDQVDRDDSDGSLDDDDVHATTEIIT	120		
Qy	121	MPETSFPLMOVDGKPKCCFFKSKIQYNKVKVAQMIYLRPVETPTTVFQILRLIKPM	180		
Db	121	MPETSFPLMOVDGKPKCCFFKSKIQYNKVKVAQMIYLRPVETPTTVFQILRLIKPM	180		
Qy	181	KDQTRYTGIRSLKLDNMPGTGIIQWSIDVKTVLQNLWKQPSNLGIEIKALDENGHDIAVT	240		
Db	181	KDQTRYTGIRSLKLDNMPGTGIIQWSIDVKTVLQNLWKQPSNLGIEIKALDENGHDIAVT	240		
Qy	241	FPQGGEDGLNPFLEVKVTDTPKSRDRDPLGDDCEHSTESCCRYPLTVDFAELGWDWIIA	300		
Db	241	FPQGGEDGLNPFLEVKVTDTPKSRDRDPLGDDCEHSTESCCRYPLTVDFAELGWDWIIA	300		
Qy	301	PKRYKANYSGCEGFVFLQYKYPHTLHVQANPRGSAGPCCTPTKMSPINMLYFNGKEQII	360		
Db	301	PKRYKANYSGCEGFVFLQYKYPHTLHVQANPRGSAGPCCTPTKMSPINMLYFNGKEQII	360		